H1CDR	(26)GFNIKDSYMH(35)
H2CDR	(50)WIDPENGDTEYAPKFQ(65)
H3CDR	(99)GTPTGPYYFDY(109)
L1CDR	(159)SASSSVSYMH(168)
L2CDR	(184)STSNLAS(190)
L3CDR	(223)QQRSSYPLT(231)

Fig. 1. Amino acid sequences of CAB1 CDRs

SEQ ID NO: 1

1	QVKLQQSGAE	LVRSGTSVKL	SCTASGFNIK	DSYMHWLRQG	PEQGLEWIGW
51	IDPENGDTEY	APKFQGKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGT
101	PTGPYYFDYW	GQGTTVTVSS	GGGGSGGGGS	GGGGSENVLT	QSPAIMSASP
151	GEKVTITCSA	SSSVSYMHWF	QQKPGTSPKL	WIYSTSNLAS	GVPARFSGSG
201	SGTSYSLTIS	RMEAEDAATY	YCQQRSSYPL	TFGAGTKLEL	KRAATPVSEK
251	QLAEVVANTI	TPLMKAQSVP	GMAVAVIYQG	KPHYYTFGKA	DIAANKPVTP
301	QTLFELGSIS	KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL	TGKQWQGIRM
351	LDLATYTAGG	LPLQVPDEVT	DNASLLRFYQ	NWQPQWKPGT	TRLYANASIG
401	LFGALAVKPS	GMPYEQAMTT	RVLKPLKLDH	TWINVPKAEE	AHYAWGYRDG
451	KAVRVSPGML	DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	SLKQGIALAQ
501	SRYWRIGSMY	QGLGWEMLNW	PVEANTVVET	SFGNVALAPL	PVAEVNPPAP
551	PVKASWVHKT	GSTGGFGSYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	LEALQ				

Fig. 2A Amino acid sequence of CAB1 protein

SEQ ID NO: 2

```
  1 TPVSEKQLAE VVANTITPLM KAQSVPGMAV AVIYQGKPHY YTFGKADIAA
 51 NKPVTPQTLF ELGSISKTFT GVLGGDAIAR GEISLDDAVT RYWPQLTGKQ
101 WQGIRMLDLA TYTAGGLPLQ VPDEVTDNAS LLRFYQNWQP QWKPGTTRLY
151 ANASIGLFGA LAVKPSGMPY EQAMTTRVLK PLKLDHTWIN VPKAEEAHYA
201 WGYRDGKAVR VSPGMLDAQA YGVKTNVQDM ANWVMANMAP ENVADASLKQ
251 GIALAQSRYW RIGSMYQGLG WEMLNWPVEA NTVVETSFGN VALAPLPVAE
301 VNPPAPPVKA SWVHKTGSTG GFGSYVAFIP EKQIGIVMLA NTSYPNPARV
351 EAAYHILEAL Q
```

Fig. 2B Amino acid sequence of BLA protein

SEQ ID NO: 3

H1CDR	(26)GFNIKDSYMH(35)
H2CDR	(50)WIDPENGDTEYAPKFQ(65)
H3CDR	(99)GLPTGPYYFDY(109)
L1CDR	(159)SASSSVSYMH(168)
L2CDR	(184)DTSNLAS(190)
L3CDR	(223)QQRDSYPLT(231)

Fig. 3A Amino acid sequences of CAB1.6 CDRs

H1CDR	(26)GFNIKDSYMH(35)
H2CDR	(50)WIDPENGDTEYAPKFQ(65)
H3CDR	(99)GLPLGAIYNDY(109)
L1CDR	(159)SASSAVYAMH(168)
L2CDR	(184)DTSNLAS(190)
L3CDR	(223)QQRDSYPLT(231)

Fig. 3B Amino acid sequences of CAB1.7 CDRs

```
  1  QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
 51  IDPENGDTEY APKFQGKATF TTDTSSNTAY LQLSSLTSED TAVYYCNEGL
101  PTGPYYFDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151  GEKVTITCSA SSSVSYMHWF QQKPGTSPKL VIYDTSNLAS GVPARFSGSG
201  SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251  QLAEVVANTI TPLMKAQSVP GMAVAVIYQG KPHYYTFGKA DIAANKPVTP
301  QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351  LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401  LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451  KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501  SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551  PVKASWVHKT GSTGGFGSYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601  LEALQ
```

Fig. 4A Amino acid sequence of CAB1.6 protein

SEQ ID NO. 7

```
  1  QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
 51  IDPENGDTEY APKFQGKATF TTDTSSNTAY LQLSSLTSED TAVYYCNEGL
101  PTGPYYFDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151  GEKVTITCSA SSSVSYMHWF QQKPGTSPKL VIYDTSNLAS GVPARFSGSG
201  SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251  QLAEVVANTI TPLMAAQSVP GMAVAVIYQG KPHYYTFGKA DIAANKPVTP
301  QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351  LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401  LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451  KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501  SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551  PVKASWVHKT GSTGGFGAYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601  LEALQ
```

Fig. 4B Amino acid sequence of CAB1.6i protein

SEQ ID NO: 8

```
  1 QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
 51 IDPENGDTEY APKFQGKATF TTDTSSNTAY LQLSSLTSED TAVYYCNEGL
101 PLGAIYNDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSAVYAMHWF QQKPGTSPKL VIYDTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMKAQSVP GMAVAVIYQG KPHYYTFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASWVHKT GSTGGFGSYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ
```

Fig. 5A Amino acid sequence of CAB1.7 protein

SEQ ID NO: 9

1	QVQLQQSGAE	LVKSGGSVKL	SCTASGFNIK	DSYMHWVRQG	PEQGLEWIGW
51	IDPENGDTEY	APKFQGKATF	TTDTSSNTAY	LQLSSLTSED	TAVYYCNEGL
101	PLGAIYNDYW	GQGTTVTVSS	GGGGSGGGGS	GGGGSENVLT	QSPAIVSASP
151	GEKVTITCSA	SSAVYAMHWF	QQKPGTSPKL	VIYDTSNLAS	GVPARFSGSG
201	SGTSYSLTIS	RMEAEDAATY	YCQQRDSYPL	TFGAGTKLEL	KRAATPVSEK
251	QLAEVVANTI	TPLMAAQSVP	GMAVAVIYQG	KPHYYTFGKA	DIAANKPVTP
301	QTLFELGSIS	KTFTGVLGGD	AIARGEISLD	DAVTRYWPQL	TGKQWQGIRM
351	LDLATYTAGG	LPLQVPDEVT	DNASLLRFYQ	NWQPQWKPGT	TRLYANASIG
401	LFGALAVKPS	GMPYEQAMTT	RVLKPLKLDH	TWINVPKAEE	AHYAWGYRDG
451	KAVRVSPGML	DAQAYGVKTN	VQDMANWVMA	NMAPENVADA	SLKQGIALAQ
501	SRYWRIGSMY	QGLGWEMLNW	PVEANTVVET	SFGNVALAPL	PVAEVNPPAP
551	PVKASWVHKT	GSTGGFGAYV	AFIPEKQIGI	VMLANTSYPN	PARVEAAYHI
601	LEALQ				

Fig. 5B Amino acid sequence of CAB1.7i protein

SEQ ID NO: 10

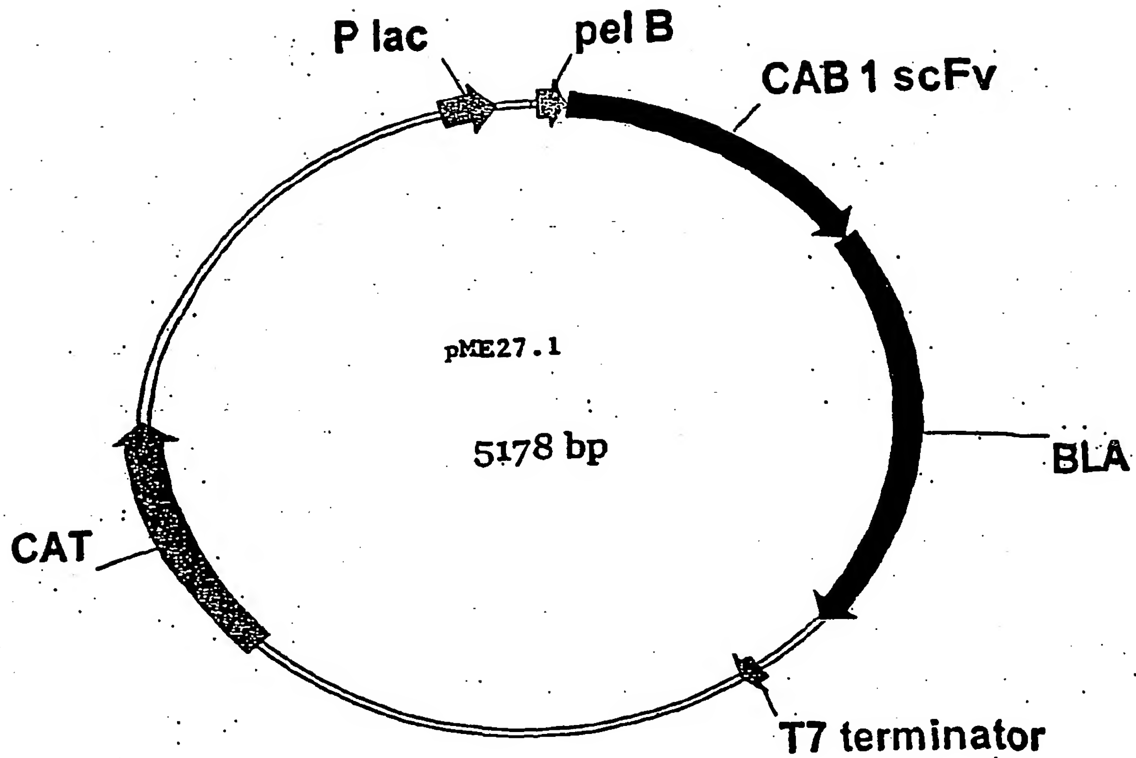


Figure 6A

```
                                                      H1                     H2
                       1                                                                              80
Translation of CAB1  (1) QVKLQQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWIDPENGDTEYAPKFQGKATFTTDTSSNTAY
human consensus      (1)  Q         KP G         TFS    V A G                      RF I R  K

                                                H3                 linker
                       81                                                                             160
Translation of CAB1 (81) LQLSSLTSEDTAVYYCNEGTPTGPYYFDYWGQGTTVTVSSGGGGSGGGGSGGGGSENVLTQSPAIMSASPGEKVTITCSA
human consensus     (81)                 AR                                    QS    P S V    QT

                        161 L1               L2                                         L3
                                                                                                      240
Translation of CAB1 (161) SSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPLTFGAGTKLELKRAA
human consensus     (161)         Y        V          D    K    A     L   E D                G
```

Figure 6B

aggaattatcatatgaaatacctgctgccgaccgctgctgctggtctgctgctcctcgctgcccagccggccatggcccaggtgaaactgcagcagt
ctggggcagaacttgtgaggtcagggacctcagtcaagttgtcctgcacagcttctggcttcaacattaaagactcctatatgcactggttgaggcagg
ggcctgaacagggcctggagtggattggatggattgatcctgagaatggtgatactgaatatgccccgaagttccagggcaaggccacttttactaca
gacacatcctccaacacagcctacctgcagctcagcagcctgacatctgaggacactgccgtctattattgtaatgaggggactccgactgggccgt
actactttgactactggggccaagggaccacggtcaccgtctcctcaggtggaggcggttcaggcggaggtggctctggcggtggcggatcagaa
aatgtgctcacccagtctccagcaatcatgtctgcatctccaggggagaaggtcaccataacctgcagtgccagctcaagtgtaagttacatgcactg
gttccagcagaagccaggcacttctcccaaactctggatttatagcacatccaacctggcttctggagtccctgctcgcttcagtggcagtggatctgg
gacctcttactctctcacaatcagccgaatggaggctgaagatgctgccacttattactgccagcaaagatctagttacccactcacgttcggtgctgg
caccaagctggagctgaaacgggcggccacaccggtgtcagaaaaacagctggcggaggtggtcgcgaatacgattaccccgctgatgaaagc
ccagtctgttccaggcatggcggtggccgttatttatcagggaaaaccgcactattacacatttggcaaggccgatatcgcggcgaataaacccgtta
cgcctcagaccctgttcgagctgggttctataagtaaaaccttcaccggcgttttaggtggggatgccattgctcgcggtgaaatttcgctggacgatg
cggtgaccagatactggccacagctgacgggcaagcagtggcagggtattcgtatgctggatctcgccacctacaccgctggcggcctgccgcta
caggtaccggatgaggtcacggataacgcctccctgctgcgcttttatcaaaactggcagccgcagtggaagcctggcacaacgcgtctttacgcca
acgccagcatcggtctttttggtgcgctggcggtcaaaccttctggcatgccctatgagcaggccatgacgacgcgggtccttaagccgctcaagct
ggaccatacctggattaacgtgccgaaagcggaagaggcgcattacgcctggggctatcgtgacggtaaagcggtgcgcgtttcgccgggtatgct
ggatgcacaagcctatggcgtgaaaaccaacgtgcaggatatggcgaactgggtcatggcaaacatggcgccggagaacgttgctgatgcctcac
ttaagcagggcatcgcgctggcgcagtcgcgctactggcgtatcgggtcaatgtatcagggtctgggctgggagatgctcaactggcccgtggagg
ccaacacggtggtcgagacgagttttggtaatgtagcactggcgccgttgcccgtggcagaagtgaatccaccggctcccccggtcaaagcgtcct
gggtccataaaacgggctctactggcgggtttggcagctacgtggcctttattcctgaaaagcagatcggtattgtgatgctcgcgaatacaagctatc
cgaacccggcacgcgttgaggcggcataccatatcctcgaggcgctacagtaggaattcgagctccgtcgacaagcttgcggccgcactcgagat
caaacgggctagccagccagaactcgccccggaagaccccgaggatgtcgagcaccaccaccaccaccactgagatccggctgctaacaaagc
ccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataaccccttggggcctctaaacgggtcttgaggggttttttgctgaaag
gaggaactatatccggattggcgaatgggacgcgccctgtagcggcgcattaagcgcggcgggtgtggtggttacgcgcagcgtgaccgctacac
ttgccagcgccctagcgcccgctcctttcgctttcttcccttcctttctcgccacgttcgccggctttccccgtcaagctctaaatcgggggctccctttag
ggttccgatttagtgctttacggcacctcgaccccaaaaaacttgattagggtgatggttcacgtagtgggccatcgccctgatagacggtttttcgccc
tttgacgttggagtccacgttctttaatagtggactcttgttccaaactggaacaacactcaaccctatctcggtctattcttttgatttataagggattttgcc
gatttcggcctattggttaaaaaatgagctgatttaacaaaaatttaacgcgaattttaacaaaatattaacgcttacaatttcctgatgcggtattttctcctt
acgcatctgtgcggtatttcacaccgcatatggtgcactctcagtacaatctgctctgatgccgcatagttaagccagccccgacacccgccaacacc
cgctgacgcgccctgacgggcttgtctgctcccggcatccgcttacagacaagctgtgaccgtctccgggagctgcatgtgtcagaggttttcaccgt
catcaccgaaacgcgcgagacgaaagggcctcgtgatacgcctatttttataggttaatgtcatgataataatggtttcttagacgtcaggtggcactttt
cggggaaatgtgcgcggaacccctatttgtttatttttctaaatacattcaaatatgtatccgctcatgagacaataaccctgtggcagcatcacccgacg
cactttgcgccgaataaatacctgtgacggaagatcacttcgcagaataaataaatcctggtgccctgttgataccgggaagccctgggccaactttt
ggcgaaaatgagacgttgatcggcacgtaagaggttccaactttcaccataatgaaataagatcactaccgggcgtattttttgagttatcgagatttca
ggagctaaggaagctaaaatggagaaaaaaatcactggatataccaccgttgatatatcccaatggcatcgtaaagaacattttgaggcatttcagtca
gttgctcaatgtacctataaccagaccgttcagctggatattacggcctttttaaagaccgtaaagaaaaataagcacaagttttatccggcctttattcac
attcttgcccgcctgatgaatgctcatccggaattccgtatggcaatgaaagacggtgagctggtgatatgggatagtgttcacccttgttacaccgtttt
ccatgagcaaactgaaacgttttcatcgctctggagtgaataccacgacgatttccggcagtttctacacatatattcgcaagatgtggcgtgttacggt
gaaaacctggcctatttccctaaagggtttattgagaatatgtttttcgtctcagccaatccctgggtgagtttcaccagttttgatttaaacgtggccaatat

Figure 6C – 1

gacaacttcttcgcccccgttttcacgatgggcaaatattatacgcaaggcgacaaggtgctgatgccgctggcgattcaggttcatcatgccgtctg
gatggcttccatgtcggcagaatgcttaatgaattacaacagtactgcgatgagtggcagggcggggcgtaaagacagatcgctgagataggtgcc
cactgattaagcattggtaactgtcagaccaagtttactcatatatactttagattgatttaaaacttcatttttaatttaaaaggatctaggtgaagatcctttt
gataatctcatgaccaaaatcccttaacgtgagttttcgttccactgagcgtcagaccccgtagaaaagatcaaaggatcttcttgagatcctttttttctg
gcgtaatctgctgcttgcaaacaaaaaaaccaccgctaccagcggtggtttgtttgccggatcaagagctaccaactctttttccgaaggtaactggc
tcagcagagcgcagataccaaatactgttcttctagtgtagccgtagttaggccaccacttcaagaactctgtagcaccgcctacatacctcgctctgc
aatcctgttaccagtggctgctgccagtggcgataagtcgtgtcttaccgggttggactcaagacgatagttaccggataaggcgcagcggtcggg
ctgaacggggggttcgtgcacacagcccagcttggagcgaacgacctacaccgaactgagatacctacagcgtgagctatgagaaagcgccacg
cttcccgaagggagaaaggcggacaggtatccggtaagcggcagggtcggaacaggagagcgcacgagggagcttccagggggaaacgcct
ggtatctttatagtcctgtcgggtttcgccacctctgacttgagcgtcgatttttgtgatgctcgtcaggggggcggagcctatggaaaaacgccagca
acgcggcctttttacggttcctggccttttgctggccttttgctcacatgttctttcctgcgttatcccctgattctgtggataaccgtattaccgcctttgagt
gagctgataccgctcgccgcagccgaacgaccgagcgcagcgagtcagtgagcgaggaagcggaagagcgcccaatacgcaaaccgcctctc
cccgcgcgttggccgattcattaatgcagctggcacgacaggtttcccgactggaaagcgggcagtgagcgcaacgcaattaatgtgagttagctca
ctcattaggcaccccaggctttacactttatgcttccggctcgtatgttgtgtggaattgtgagcggataacaatttcacacaggaaacagctatgaccat
gattacgccaagctatttaggtgacactatagaatactcaagctttctagattaagg

Figure 6C -2

heavy chain:
qvklqqsgaelvrsgtsvklsctasgfnikdsymhwlrqgpeqglewigwidpengdteyapkfqgkatfttdtssntaylqlssltsedtavyycnegtptgpyyfdywgqgttvtvss

linker:
ggggsggggsggggs

light chain:
envltqspaimsaspgekvtitcsasssvsymhwfqqkpgtspklwiystsnlasgvparfsgsgsgtsysltisrmeaedaatyycqqrssypltfgagtklelkraat

BLA:
pvsekqlaevvantitplmkaqsvpgmavaviyqgkphyytfgkadiaankpvtpqtlfelgsisktftgvlggdaiargeislddavtrywpqltgkqwqgirmldlatytagglplqvpdevtd
nasllrfyqnwqpqwkpgttrlyanasiglfgalavkpsgmpyeqamttrvlkplkldhtwinvpkaeeahyawgyrdgkavrvspgmldaqaygvktnvqdmanwvmanmapenva
daslkqgialaqsrywrigsmyqglgwemlnwpveantvvetsfgnvalaplpvaevnppappvkaswvhktgstggfgsyvafipekqigivmlantsypnparveaayhilealq

Figure 6D

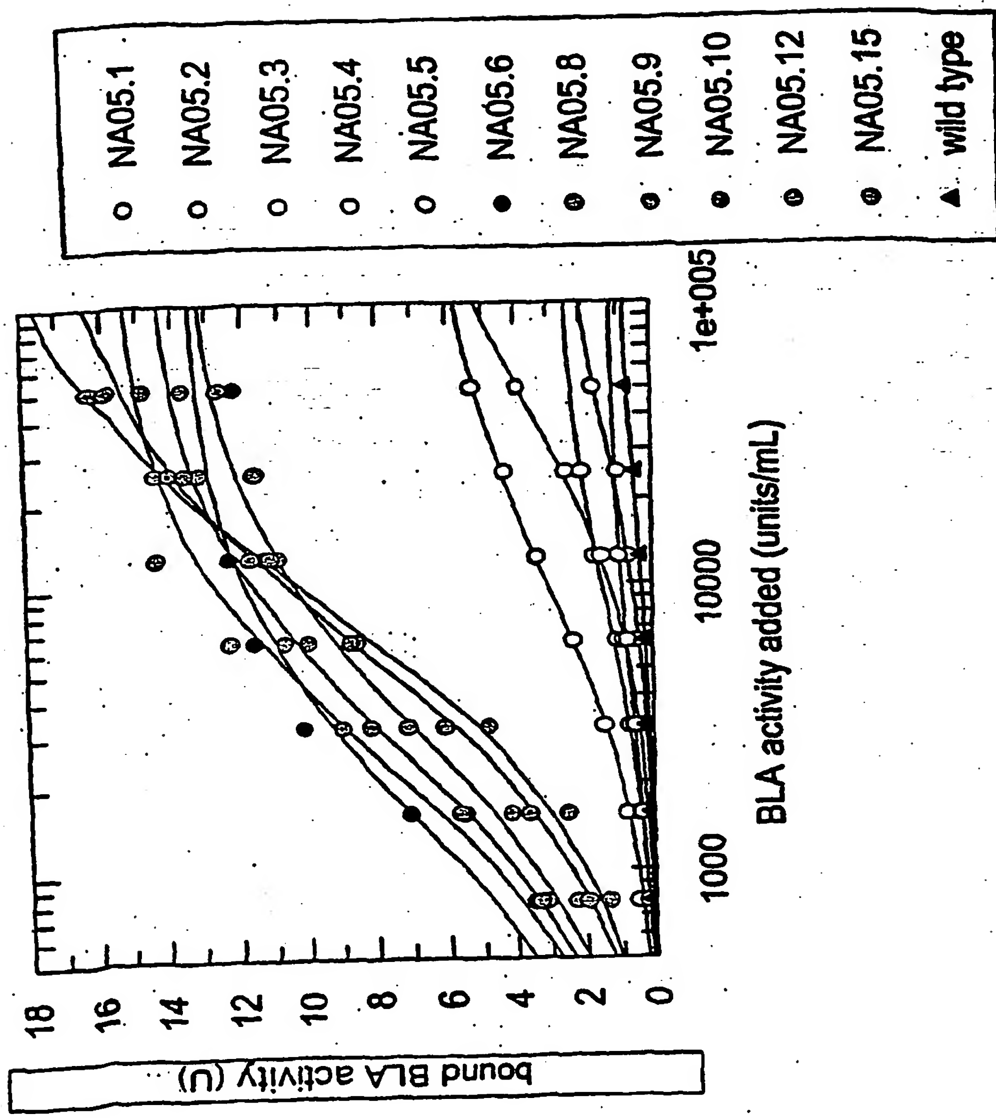

NA05.1
NA05.2
NA05.3
NA05.4
NA05.5
NA05.6
NA05.8
NA05.9
NA05.10
NA05.12
NA05.15
wild type
bound BLA activity (U)
0
2
4
6
8
10
12
14
16
18
1000
10000
1e+005
BLA activity added (units/mL)

Figure7A

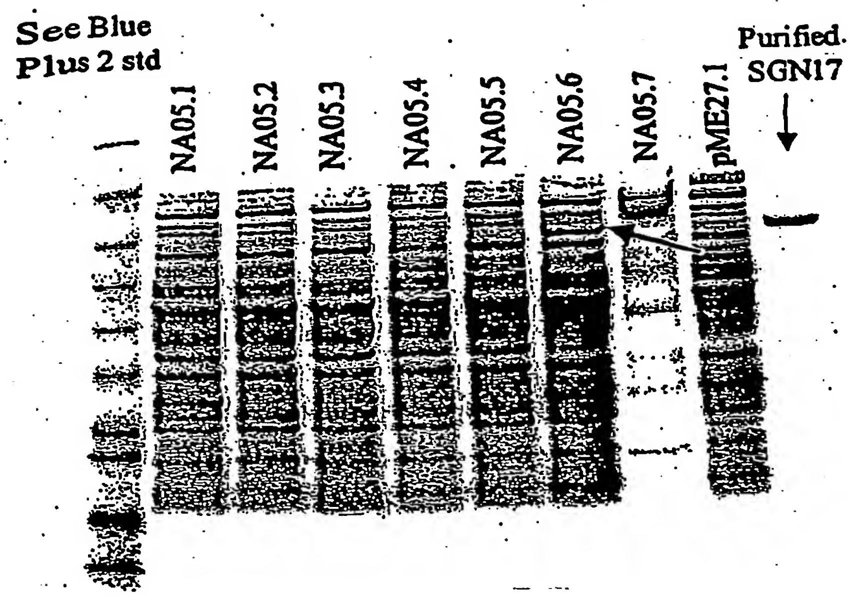

See Blue
Plus 2 std
NA05.1
NA05.2
NA05.3
NA05.4
NA05.5
NA05.6
NA05.7
pME27.1
Purified
SGN17

Figure 7B

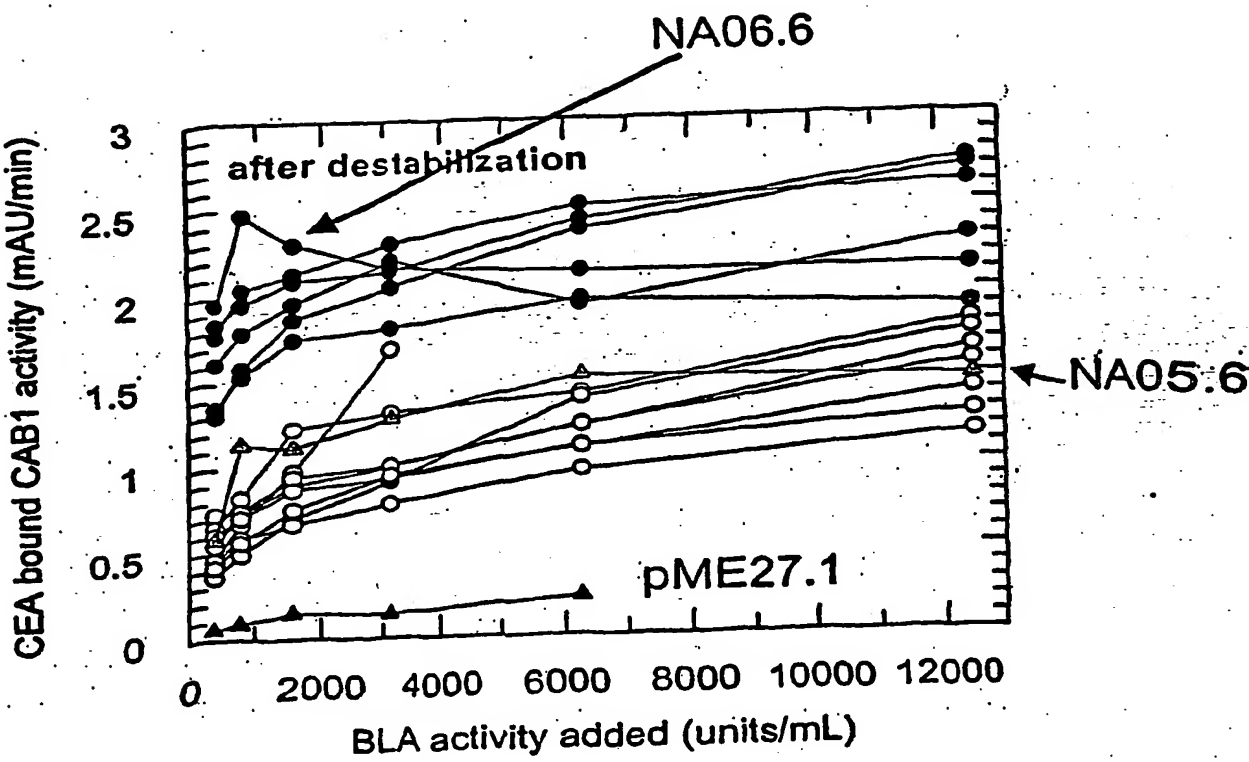

NA06.6
after destabilization
NA05.6
pME27.1
CEA bound CAB1 activity (mAU/min)
3
2.5
2
1.5
1
0.5
0
0
2000
4000
6000
8000
10000
12000
BLA activity added (units/mL)

Figure 7C

pos. heavy chain	number of observations	observed frequencies of 5 most abundend amio acids in alignment of human sequenes										CAB1 sequence	CDR	mutated residues
1	291	E	0.616	Q	0.346	D	0.014	G	0.014	A	0.003	L	0.003	Q		
2	293	V	0.887	M	0.027	L	0.024	S	0.020	I	0.017	A	0.007	V		
3	291	Q	0.852	H	0.034	R	0.027	T	0.027	E	0.014	V	0.014	K		1
4	282	L	0.975	V	0.011	A	0.007	D	0.004	M	0.004			L		
5	276	V	0.645	Q	0.148	L	0.120	R	0.022	M	0.014	N	0.014	Q		
6	267	E	0.693	Q	0.263	A	0.022	D	0.011	G	0.007	R	0.004	Q		
7	265	S	0.951	W	0.019	X	0.015	T	0.008	A	0.004	N	0.004	S		
8	266	G	0.989	S	0.008	T	0.004							G		
9	274	G	0.624	A	0.193	P	0.164	S	0.011	E	0.004	H	0.004	A		
10	271	G	0.638	E	0.192	D	0.081	A	0.070	T	0.011	V	0.007	E		
11	270	L	0.681	V	0.270	F	0.030	S	0.019					L		
12	267	V	0.757	K	0.154	I	0.026	N	0.022	L	0.015	A	0.007	V		
13	247	K	0.474	Q	0.428	R	0.049	E	0.034	G	0.004	H	0.004	R		1
14	251	P	0.968	A	0.012	K	0.008	G	0.004	L	0.004	S	0.004	S		1
15	244	G	0.783	S	0.156	T	0.033	P	0.016	K	0.008	E	0.004	G		
16	243	G	0.488	E	0.131	Q	0.107	A	0.094	R	0.082	S	0.066	T		1
17	234	S	0.766	T	0.204	A	0.009	F	0.009	P	0.004	R	0.004	S		
18	244	L	0.812	V	0.155	M	0.008	A	0.004	E	0.004	F	0.004	V		
19	242	R	0.545	K	0.240	S	0.161	T	0.037	A	0.012	Q	0.004	K		
20	246	L	0.736	V	0.191	I	0.061	E	0.004	R	0.004	X	0.004	L		
21	218	S	0.729	T	0.234	G	0.009	I	0.009	A	0.005	D	0.005	S		
22	217	C	0.991	R	0.005	S	0.005							C		
23	231	A	0.558	K	0.203	T	0.117	E	0.048	V	0.022	I	0.013	T		
24	235	A	0.638	V	0.174	G	0.064	I	0.055	T	0.030	F	0.026	A		
25	226	S	0.951	Y	0.027	F	0.009	C	0.004	K	0.004	T	0.004	S		
26	225	G	0.956	E	0.013	A	0.009	D	0.009	S	0.009	V	0.004	G		
27	213	F	0.559	Y	0.164	G	0.150	D	0.080	S	0.019	L	0.014	F		
28	203	T	0.571	S	0.286	I	0.049	N	0.049	P	0.015	A	0.005	N		1
29	207	F	0.749	V	0.111	I	0.068	L	0.053	T	0.010	A	0.005	I		1
30	202	S	0.762	T	0.119	N	0.035	G	0.020	R	0.020	A	0.010	K		1
31	199	S	0.482	T	0.136	D	0.104	N	0.087	G	0.060	K	0.040	D	H1	
32	202	Y	0.535	S	0.144	N	0.083	A	0.069	D	0.031	G	0.030	S	H1	
33	197	A	0.269	Y	0.162	G	0.147	W	0.117	S	0.091	T	0.066	Y	H1	
34	200	M	0.520	I	0.210	W	0.070	A	0.055	Y	0.050	V	0.040	M	H1	
35	196	S	0.372	H	0.235	N	0.077	A	0.061	G	0.051	Y	0.046	H	H1	
35a	33	-	0.824	W	0.096	V	0.043	G	0.016	S	0.016	N	0.005		H2	
35b	27	-	0.856	N	0.064	G	0.037	S	0.032	A	0.005	R	0.005		H3	
36	192	W	0.990	M	0.005	T	0.005							W		
37	193	V	0.741	I	0.228	L	0.021	G	0.005	Q	0.005			L		1
38	190	R	0.989	P	0.005	V	0.005							R		
39	190	Q	0.979	T	0.011	G	0.005	R	0.005					Q		
40	191	A	0.634	P	0.199	S	0.073	M	0.052	G	0.010	V	0.010	G		1
41	187	P	0.914	S	0.043	T	0.021	A	0.005	L	0.005	Q	0.005	P		
42	187	G	0.925	S	0.064	P	0.005	R	0.005					E		1
43	186	K	0.683	Q	0.183	R	0.124	E	0.005	H	0.005			Q		
44	186	G	0.882	A	0.048	S	0.043	R	0.027					G		
45	186	L	0.978	P	0.022									L		
46	185	E	0.956	Q	0.039	V	0.005							E		
47	184	W	0.989	S	0.011									W		

Figure 8A — 1

48	185	V	0.481	M	[illegible]	I	0.173	L	0.124					I		
49	185	G	0.600	S	0.216	A	0.162	E	0.005	L	0.005	[illegible]	0.005	G		
50	185	R	0.146	W	0.146	V	0.119	A	0.114	G	0.081	Y	0.081	W	H2	
51	185	I	0.822	T	0.081	R	0.027	V	0.022	K	0.016	M	0.011	I	H2	
52	184	S	0.250	Y	0.239	N	0.123	K	0.060	I	0.054	D	0.050	D	H2	
52a	141	-	0.230	P	0.180	Y	0.153	G	0.126	N	0.068	V	0.055	P	H2	
52b	34	-	0.814	K	0.115	R	0.060	G	0.005	Y	0.005				H2	
52c	22	-	0.880	T	0.044	V	0.033	S	0.022	A	0.011	G	0.005		H2	
53	184	S	0.228	D	0.163	Y	0.125	G	0.109	N	0.082	H	0.054	E	H2	
54	183	G	0.328	S	0.202	D	0.129	N	0.112	K	0.082	F	0.055	N	H2	
55	182	G	0.544	S	0.181	D	0.085	W	0.066	Y	0.060	N	0.020	G	H2	
56	182	S	0.231	D	0.182	N	0.147	T	0.143	Y	0.077	G	0.060	D	H2	
57	184	T	0.582	K	0.120	N	0.065	A	0.054	I	0.054	P	0.022	T	H2	
58	183	Y	0.322	N	0.216	D	0.139	R	0.060	H	0.055	T	0.038	E	H2	
59	184	Y	0.908	F	0.043	N	0.016	S	0.011	D	0.005	G	0.005	Y	H2	
60	183	A	0.579	N	0.153	S	0.104	T	0.055	R	0.044	G	0.027	A	H2	
61	184	D	0.277	P	0.239	Q	0.174	A	0.141	V	0.076	T	0.033	P	H2	
62	185	S	0.686	K	0.146	P	0.065	N	0.038	G	0.016	R	0.016	K	H2	
63	186	V	0.511	L	0.247	F	0.215	S	0.011	A	0.005	K	0.005	F	H2	
64	186	K	0.581	Q	0.274	R	0.054	N	0.032	E	0.022	T	0.022	Q	H2	
65	186	G	0.688	S	0.237	T	0.032	A	0.016	D	0.011	E	0.011	G	H2	
66	186	R	0.935	Q	0.054	H	0.005	I	0.005					K		1
67	186	F	0.462	V	0.409	I	0.065	L	0.054	A	0.005	S	0.005	A		1
68	186	T	0.914	I	0.038	A	0.016	S	0.011	K	0.005	N	0.005	T		
69	187	I	0.791	M	0.139	V	0.032	D	0.005	F	0.005	G	0.005	F		1
70	187	S	0.684	T	0.214	N	0.070	L	0.032					T		
71	187	R	0.529	V	0.160	A	0.107	P	0.064	T	0.053	K	0.043	T		1
72	186	D	0.902	N	0.071	K	0.016	E	0.011					D		
73	185	T	0.368	N	0.266	D	0.177	K	0.070	E	0.059	A	0.011	T		
74	186	S	0.946	A	0.048	L	0.005							S		
75	187	K	0.674	T	0.139	I	0.070	R	0.027	A	0.021	F	0.021	S		1
76	187	N	0.701	S	0.251	K	0.027	R	0.011	T	0.005	Y	0.005	N		
77	187	T	0.615	Q	0.273	S	0.048	M	0.021	L	0.016	P	0.011	T		
78	186	L	0.364	A	0.273	F	0.235	V	0.096	I	0.005	M	0.005	A		
79	187	Y	0.638	S	0.239	F	0.059	V	0.048	H	0.005	M	0.005	Y		
80	187	L	0.782	M	0.207	N	0.005	-	0.005					L		
81	187	Q	0.529	E	0.205	K	0.122	R	0.032	T	0.032	N	0.027	Q		
82	194	M	0.497	L	0.421	W	0.051	V	0.015	I	0.010	-	0.005	L		
82a	195	N	0.442	S	0.291	R	0.077	T	0.066	D	0.053	G	0.020	S		
82b	194	S	0.795	N	0.082	R	0.051	G	0.026	T	0.021	A	0.010	S		
82c	197	L	0.701	V	0.234	M	0.041	G	0.010	A	0.005	D	0.005	L		
83	197	R	0.528	T	0.239	K	0.122	D	0.041	E	0.020	Q	0.015	T		
84	198	A	0.495	P	0.182	S	0.177	T	0.051	I	0.035	V	0.030	S		
85	198	E	0.591	A	0.172	D	0.126	S	0.051	V	0.045	G	0.015	E		
86	198	D	0.975	T	0.010	V	0.010	N	0.005					D		
87	198	T	0.929	S	0.035	G	0.010	M	0.010	A	0.005	Q	0.005	T		
88	198	A	0.939	G	0.040	P	0.005	T	0.005	V	0.005	Y	0.005	A		
89	198	V	0.768	L	0.066	M	0.056	T	0.045	I	0.040	F	0.010	V		
90	199	Y	0.980	F	0.010	A	0.005	I	0.005					Y		
91	199	Y	0.930	F	0.045	C	0.015	R	0.005	T	0.005			Y		
92	198	C	0.990	A	0.005	M	0.005							C		
93	198	A	0.838	T	0.076	V	0.061	H	0.005	K	0.005	N	0.005	N		1
94	198	R	0.596	K	0.162	T	0.051	G	0.045	P	0.045	Q	0.025	E		1
95	161	G	0.174	D	0.120	E	0.099	A	0.093	N	0.092	P	0.068	G		
96	159	P	0.168	R	0.130	G	0.112	L	0.062	V	0.062	Y	0.062	T	H3	
97	156	G	0.170	P	0.094	V	0.094	E	0.088	T	0.069	S	0.063	P	H3	
98	155	G	0.152	Y	0.101	L	0.095	D	0.087	V	0.076	S	0.063	T	H3	

Figure 8A -2

pos. light chain	number of observations	observed frequencies of 5 most abundand amio acids in alignment of human sequenes												CAB1 sequence	CDR	mutated residues
1	95	Q	0.589	S	0.158	N	0.095	H	0.074	D	0.053	F	0.021	E		1
2	139	S	0.446	Y	0.388	F	0.101	V	0.043	L	0.014	T	0.007	N		1
3	140	V	0.307	E	0.243	A	0.207	M	0.093	D	0.064	I	0.043	V		
4	140	L	0.971	V	0.029									L		
5	141	T	0.915	A	0.021	S	0.021	I	0.014	K	0.007	L	0.007	T		
6	140	Q	0.993	E	0.007									Q		
7	139	P	0.906	D	0.029	S	0.029	A	0.022	E	0.014			S		1
8	139	P	0.741	A	0.137	H	0.072	R	0.029	L	0.007	S	0.007	P		
9	139	S	0.964	A	0.014	V	0.014	R	0.007					A		1
10	0	-	1.000											I		1
11	138	V	0.790	A	0.138	L	0.058	M	0.014					M		1
12	139	S	0.978	F	0.007	T	0.007	E	0.004	Q	0.004			S		
13	138	V	0.406	G	0.348	A	0.138	E	0.087	L	0.014	D	0.007	A		
14	135	S	0.630	A	0.230	T	0.111	D	0.007	F	0.007	G	0.007	S		
15	135	P	0.881	L	0.089	A	0.022	S	0.007					P		
16	134	G	0.978	E	0.015	L	0.007							G		
17	133	Q	0.811	K	0.098	A	0.045	E	0.024	G	0.015	H	0.008	E		1
18	133	T	0.504	S	0.263	R	0.135	K	0.068	E	0.008	G	0.008	K		1
19	130	V	0.454	A	0.385	I	0.146	G	0.008	L	0.008			V		
20	128	T	0.531	R	0.188	S	0.148	K	0.047	I	0.031	M	0.016	T		
21	121	I	0.901	V	0.050	L	0.017	A	0.008	F	0.008	M	0.008	I		
22	120	S	0.492	T	0.475	A	0.008	G	0.008	I	0.008	N	0.008	T		
23	117	C	1.000											C		
24	112	S	0.536	T	0.259	G	0.089	A	0.045	Q	0.033	I	0.018	S	L1	
25	108	G	0.870	L	0.056	R	0.028	A	0.019	I	0.009	P	0.009	A	L1	
26	108	D	0.339	S	0.250	T	0.213	N	0.087	E	0.037	G	0.037	S	L1	
27	104	S	0.415	N	0.118	K	0.113	A	0.104	T	0.066	G	0.047	S	L1	
28	104	L	0.346	S	0.346	I	0.115	G	0.067	A	0.058	D	0.019	S	L1	
29	100	G	0.243	N	0.239	D	0.159	S	0.078	P	0.068	H	0.058	V	L1	
30	103	I	0.291	V	0.165	D	0.136	N	0.107	E	0.058	S	0.049	S	L1	
31	101	G	0.356	K	0.168	A	0.099	E	0.084	Q	0.084	D	0.069	Y	L1	
31a	54	-	0.438	S	0.167	G	0.104	N	0.083	Y	0.063	D	0.052	M	L1	
31b	49	-	0.495	N	0.227	Y	0.155	S	0.041	G	0.021	H	0.021	H	L1	
31c	23	-	0.760	N	0.134	S	0.031	K	0.021	D	0.012	E	0.010		L1	
31d	0	-	1.000												L1	
31e	0	-	1.000												L1	
31f	0	-	1.000												L1	
32	94	Y	0.515	S	0.134	F	0.093	A	0.072	T	0.052	H	0.041		L1	
33	97	V	0.680	A	0.186	I	0.082	Y	0.021	F	0.010	P	0.010		L1	
34	92	S	0.380	H	0.120	A	0.109	Y	0.098	N	0.076	Q	0.076		L1	
35	98	W	0.990	Y	0.010									W		
36	96	Y	0.844	F	0.073	H	0.073	W	0.010					F		1
37	95	Q	0.916	R	0.042	E	0.011	H	0.011	K	0.011	Y	0.011	Q		
38	94	Q	0.862	H	0.053	L	0.053	E	0.011	K	0.011	V	0.011	Q		
39	93	K	0.333	L	0.172	R	0.161	H	0.151	Q	0.086	V	0.043	K		
40	93	P	0.946	S	0.022	A	0.011	L	0.011	R	0.011			P		

Figure 8B -1

41	93	G	0.871	H	[illegible]	D	0.022	R	0.022	P	[illegible]	[illegible]	0.011	G		
42	92	Q	0.424	T	0.217	K	0.163	R	0.087	S	0.0[illegible]	G	0.022	T		
43	92	A	0.717	S	0.174	G	0.065	T	0.022	L	0.011	V	0.011	S		
44	93	P	0.978	A	0.011	M	0.011							P		
45	92	K	0.391	V	0.315	R	0.109	L	0.065	T	0.065	A	0.033	K		
46	92	L	0.728	V	0.076	F	0.065	T	0.043	A	0.022	M	0.022	L		
47	91	V	0.484	L	0.374	I	0.077	M	0.055	N	0.011			W		1
48	91	I	0.791	V	0.110	M	0.077	L	0.011	S	0.011			I		
49	91	Y	0.769	F	0.110	R	0.066	H	0.022	D	0.011	I	0.011	Y		
50	89	D	0.303	E	0.210	Q	0.093	V	0.067	G	0.056	K	0.056	S	L2	
51	88	D	0.364	N	0.205	V	0.159	H	0.068	T	0.068	G	0.034	T	L2	
52	89	N	0.393	T	0.213	S	0.202	D	0.101	A	0.022	F	0.011	S	L2	
53	88	K	0.307	D	0.193	Q	0.182	N	0.080	E	0.057	S	0.057	N	L2	
54	88	R	0.875	X	0.068	K	0.034	L	0.011	W	0.011			L	L2	
55	86	P	0.851	G	0.080	S	0.023	A	0.011	H	0.011	R	0.011	A	L2	
56	85	S	0.837	D	0.081	P	0.023	A	0.012	L	0.012	T	0.012	S	L2	
57	86	G	0.920	E	0.034	S	0.011	T	0.011	W	0.011	-	0.011	G		
58	84	I	0.600	V	0.353	A	0.012	G	0.012	T	0.012	-	0.012	V		
59	84	P	0.847	S	0.106	A	0.012	L	0.012	V	0.012	-	0.012	P		
60	85	D	0.488	E	0.325	N	0.047	A	0.035	H	0.023	L	0.023	A		1
61	87	R	0.977	D	0.011	-	0.011							R		
62	88	F	0.943	I	0.034	L	0.011	R	0.011					F		
63	87	S	0.989	F	0.011									S		
64	87	G	0.885	A	0.069	S	0.023	V	0.023					G		
65	87	S	0.977	G	0.011	Y	0.011							S		
66	86	K	0.430	N	0.186	S	0.186	T	0.081	X	0.070	R	0.035	G		1
67	85	S	0.953	T	0.024	K	0.012	L	0.012					S		
68	85	G	0.859	S	0.071	A	0.035	D	0.024	Q	0.012			G		
69	85	N	0.434	T	0.318	A	0.129	D	0.036	G	0.024	K	0.024	T		
70	85	T	0.529	S	0.341	E	0.082	A	0.024	K	0.024			S		
71	85	A	0.847	R	0.082	V	0.059	S	0.012					Y		1
72	85	T	0.447	S	0.424	Y	0.082	A	0.035	I	0.012			S		
73	85	L	0.988	S	0.012									L		
74	85	T	0.706	A	0.165	G	0.106	I	0.012	L	0.012			T		
75	85	I	0.929	V	0.047	A	0.012	L	0.012					I		
76	85	S	0.718	T	0.200	N	0.035	I	0.024	G	0.012	R	0.012	S		
77	85	G	0.765	R	0.129	S	0.094	E	0.012					R		
78	85	L	0.588	V	0.224	T	0.106	A	0.071	G	0.012			M		1
79	85	Q	0.659	E	0.153	R	0.071	K	0.047	L	0.024	A	0.012	E		
80	85	A	0.459	S	0.235	T	0.200	V	0.047	P	0.035	N	0.012	A		
81	85	E	0.541	G	0.235	M	0.071	D	0.047	L	0.024	N	0.024	E		
82	85	D	0.964	N	0.024	E	0.012							D		
83	85	E	0.976	D	0.012	T	0.012							A		1
84	85	A	0.941	T	0.035	E	0.012	S	0.012					A		
85	85	D	0.859	E	0.082	H	0.024	A	0.012	I	0.012	M	0.012	T		1
86	85	Y	0.976	F	0.012	H	0.012							Y		
87	85	Y	0.894	F	0.106									Y		
88	85	C	0.988	H	0.012									C		
89	85	Q	0.482	A	0.153	S	0.141	G	0.094	C	0.059	N	0.035	Q	L3	
90	85	Q	0.388	T	0.271	A	0.212	V	0.118	L	0.012			Q	L3	
91	85	S	0.576	Y	0.247	A	0.059	F	0.035	R	0.035	D	0.012	R	L3	
92	84	W	0.606	G	0.095	A	0.071	N	0.061	T	0.048	E	0.024	S	L3	
93	84	D	0.405	D	0.179	G	0.107	N	0.095	P	0.071	T	0.060	S	L3	
94	84	S	0.536	G	0.155	N	0.073	R	0.060	D	0.058	T	0.048	Y	L3	
95	82	S	0.265	L	0.253	G	0.108	N	0.096	T	0.084	A	0.036	P	L3	

Figure 8B - 2

95a	60	-	0.268	S	0.183	D	0.159	N	0.110	T	0.073	Q	0.049	L	L3	
95b	40	-	0.512	A	0.098	G	0.098	H	0.085	E	0.049	R	0.037	T	L3	
95c	5	-	0.939	P	0.037	A	0.012	G	0.012						L3	
95d	1	-	0.988	G	0.012										L3	
95e	0	-	1.000												L3	
95f	0	-	1.000												L3	
96	80	V	0.305	G	0.098	P	0.098	W	0.098	A	0.073	N	0.073		L3	
97	85	V	0.788	I	0.118	L	0.047	M	0.035	G	0.012				L3	
98	86	F	0.988	V	0.012									F		
99	89	G	0.989	F	0.011									G		
100	89	G	0.831	T	0.124	A	0.022	S	0.022					A		1
101	89	G	1.000											G		
102	89	T	0.989	G	0.011									T		
103	88	K	0.739	N	0.091	R	0.068	Q	0.034	T	0.034	E	0.011	K		
104	87	L	0.667	V	0.322	Q	0.011							L		
105	87	T	0.954	S	0.023	I	0.011	L	0.011					E		1
106	85	V	0.988	T	0.012									L		1
106a	84	L	0.952	V	0.024	P	0.012	Q	0.012					K		1
107	78	G	0.782	S	0.103	R	0.090	C	0.013	L	0.013			R		1
108	46	Q	0.957	P	0.022	R	0.022							A		1
109	46	P	0.957	K	0.022	Q	0.022							A		1

Figure 8B ~3

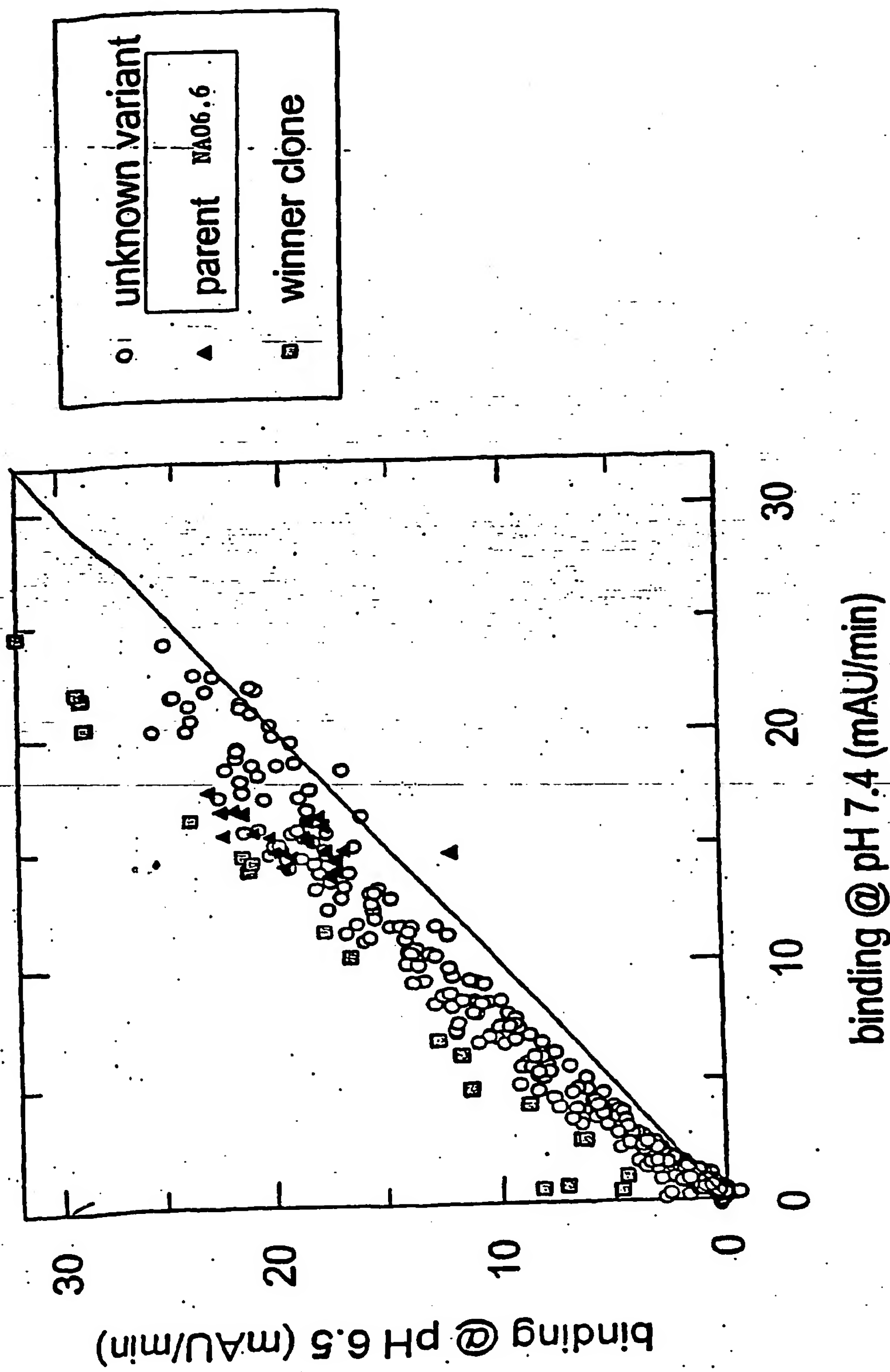

unknown variant
parent
NA06.6
winner clone
binding @ pH 7.4 (mAU/min)
binding @ pH 6.5 (mAU/min)
0
10
20
30
0
10
20
30

Figure 9

CDRs in NA06.6

Residues chosen for mutagenesis in NA06.6

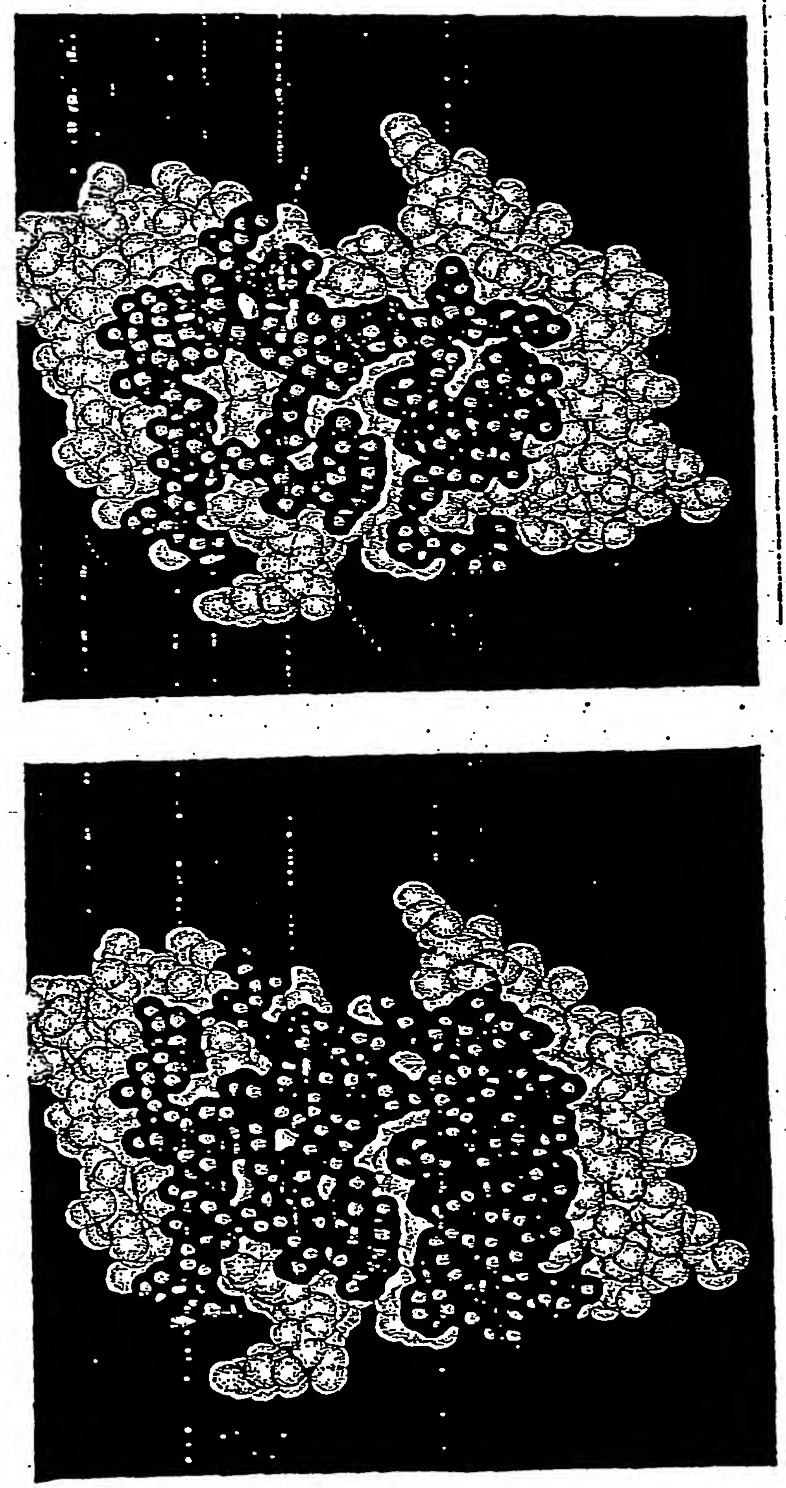


Figure 10

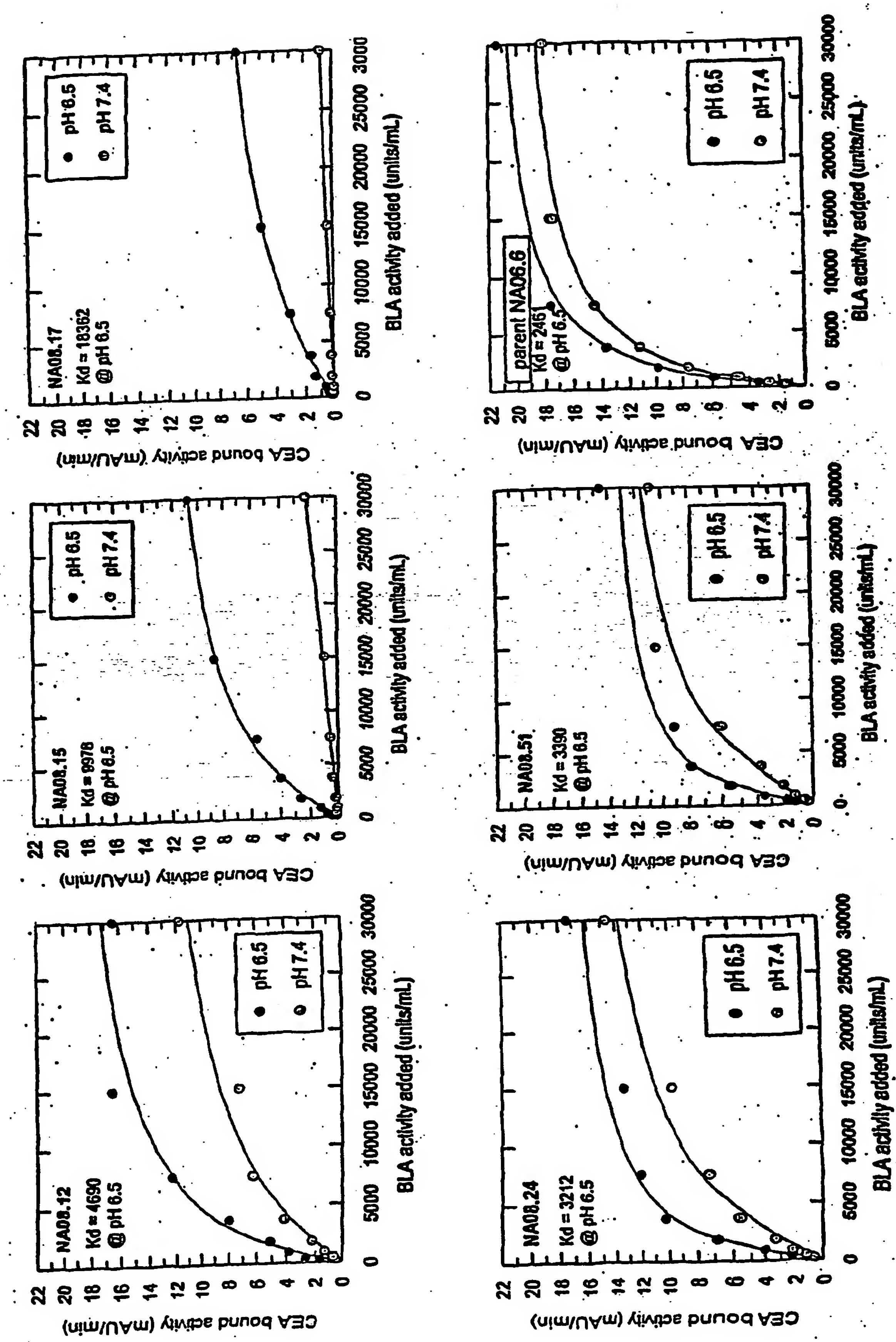

NA08.17
Kd = 18362
@ pH 6.5
NA08.15
Kd = 9978
@ pH 6.5
NA08.12
Kd = 4690
@ pH 6.5
parent NA06.6
Kd = 2461
@ pH 6.5
NA08.51
Kd = 3390
@ pH 6.5
NA08.24
Kd = 3212
@ pH 6.5
pH 6.5
pH 7.4
CEA bound activity (mAU/min)
BLA activity added (units/mL)

Figure 11

Figure 12: CAB1 engineering - summary

protein	changes	comments
CAB1	parent	
CAB1.1(NA05.6)	R13K, T16G, W181V	increase stability
CAB1.2(NA06.6)	K3Q, L37V, M146V	increase stability
CAB1.4(NA08.15)	S184D, S226D	pH-dependent binding
CAB1.6	T100L	increased affinity
SW149.5	T102L, P104A, Y105I, F107N	increased affinity
CAB1.7	S163T, S165Y, Y166S	increased affinity
CAB1.7I	in BLA: K265A, S568A	remove T-cell epitopes

cumulative changes

Figure 13: Binding of various CAB1 variants to immobilized CEA

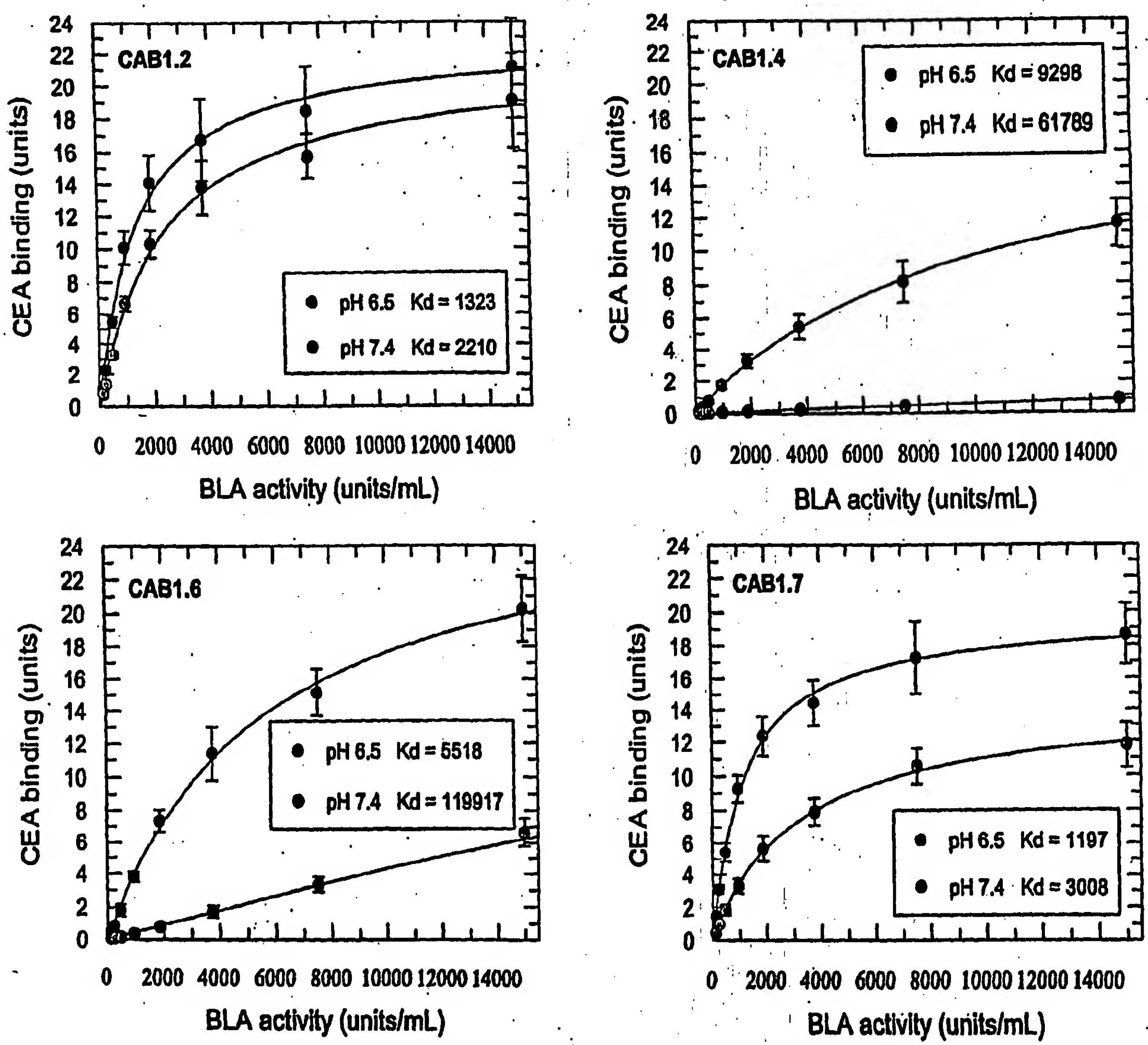
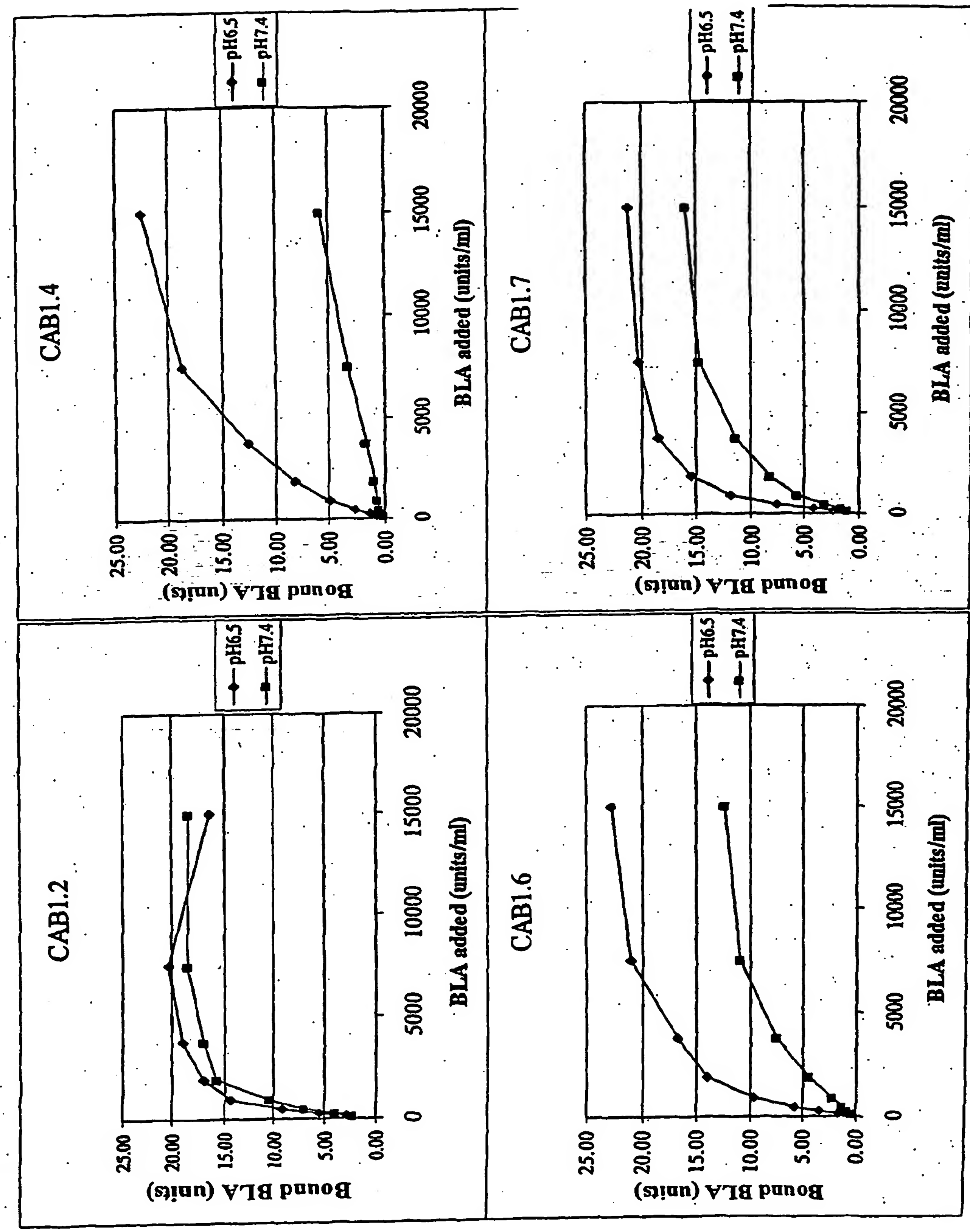


Figure 14: Binding of various CAB1 variants to LS174T cells



1 QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
51 IDPENGDTEY APKFQGKATF TTDTSSNTAY LQLSSLTSED TAVYYCNEGL
101 PLGAIYNDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSSVSYMHWF QQKPGTSPKL VIYDTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMKAQSVP GMAVAVIYQG KPHYYTFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASWVHKT GSTGGFGSYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ

Fig. 15A Amino acid sequence of SW149.5 protein

```
  1  QVKLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWLRQG PEQGLEWIGW
 51  IDPENGDTEY APKFQGKATF TTDTSSNTAY LQLSSLTSED TAVYYCNEGT
101  PTGPYYFDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIMSASP
151  GEKVTITCSA SSSVSYMHWF QQKPGTSPKL VIYSTSNLAS GVPARFSGSG
201  SGTSYSLTIS RMEAEDAATY YCQQRSSYPL TFGAGTKLEL KRAATPVSEK
251  QLAEVVANTI TPLMKAQSVP GMAVAVIYQG KPHYYTFGKA DIAANKPVTP
301  QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351  LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401  LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451  KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501  SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551  PVKASWVHKT GSTGGFGSYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601  LEALQ
```

Fig. 15B Amino acid sequence of CAB1.1 protein

```
   1 CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
  51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
 101 TGCACTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
 151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
 201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
 251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGACT
 301 CCGACTGGGC CGTACTACTT TGACTACTGG GGCCAAGGGA CCACGGTCAC
 351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
 401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
 451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
 501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAACTC GTGATTTATA
 551 GCACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
 601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
 651 TGCCACTTAT TACTGCCAGC AAAGATCTAG TTACCCACTC ACGTTCGGTG
 701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
 751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGAAAGCCCA
 801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
 851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
 901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
 951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGAA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG
```

Fig. 15C Nucleotide sequence of CAB1.2 gene

```
  1  QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
 51  IDPENGDTEY APKFQGKATF TTDTSSNTAY LQLSSLTSED TAVYYCNEGT
101  PTGPYYFDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151  GEKVTITCSA SSSVSYMHWF QQKPGTSPKL VIYSTSNLAS GVPARFSGSG
201  SGTSYSLTIS RMEAEDAATY YCQQRSSYPL TFGAGTKLEL KRAATPVSEK
251  QLAEVVANTI TPLMKAQSVP GMAVAVIYQG KPHYYTFGKA DIAANKPVTP
301  QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351  LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401  LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451  KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501  SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551  PVKASWVHKT GSTGGFGSYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601  LEALQ
```

Fig. 15D Amino acid sequence of CAB1.2 protein

H1CDR	(26)GFNIKDSYMH(35)
H2CDR	(50)WIDPENGDTEYAPKFQ(65)
H3CDR	(99)GTPTGPYYFDY(109)
L1CDR	(159)SASSSVSYMH(168)
L2CDR	(184)DTSNLAS(190)
L3CDR	(223)QQRDSYPLT(231)

Fig. 15E Amino acid sequences of CAB1.4 CDRs

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC (183)

H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)

H3CDR (373) GGGACTCCGACTGGGCCGTACTACTTTGACTAC (405)

L1CDR (553) AGTGCCAGCTCAAGTGTAAGTTACATGCAC (582)

L2CDR (628) GATACATCCAACCTGGCTTCT (648)

L3CDR (745) CAGCAAAGAGATAGTTACCCACTCACG (771)

Fig. 15F Nucleotide sequence of CAB1.4 CDRs

1 CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCACTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGACT
301 CCGACTGGGC CGTACTACTT TGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAACTC GTGATTTATG
551 ATACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGAAAGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGAA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG

Fig. 15G. Nucleotide sequence of CAB1.4 gene

```
  1 QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
 51 IDPENGDTEY APKFQGKATF TTDTSSNTAY LQLSSLTSED TAVYYCNEGT
101 PTGPYYFDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSSVSYMHWF QQKPGTSPKL VIYDTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMKAQSVP GMAVAVIYQG KPHYYTFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASWVHKT GSTGGFGSYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ
```

Fig. 15H Amino acid sequence of CAB1.4 protein

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC (183)

H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)

H3CDR (373) GGGCTCCCGACTGGGCCGTACTACTTTGACTAC (405)

L1CDR (553) AGTGCCAGCTCAAGTGTAAGTTACATGCAC (582)

L2CDR (628) GATACATCCAACCTGGCTTCT (648)

L3CDR (745) CAGCAAAGAGATAGTTACCCACTCACG (771)

Fig. 15I Nucleotide sequences of CAB1.6 CDRs

```
   1 CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
  51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
 101 TGCACTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
 151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
 201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
 251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGCTC
 301 CCGACTGGGC CGTACTACTT TGACTACTGG GGCCAAGGGA CCACGGTCAC
 351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
 401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
 451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
 501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAACTC GTGATTTATG
 551 ATACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
 601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
 651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
 701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
 751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGAAAGCCCA
 801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
 851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
 901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
 951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGAA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG
```

Fig. 15J Nucleotide sequence of CAB1.6 gene

```
1     CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51    AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101   TGCACTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151   ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
201   GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251   GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGCTC
301   CCGACTGGGC CGTACTACTT TGACTACTGG GGCCAAGGGA CCACGGTCAC
351   CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401   GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451   GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
501   GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAACTC GTGATTTATG
551   ATACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601   TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651   TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
701   CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751   CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGGCGGCCCA
801   GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851   ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901   CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951   AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001  CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051  CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101  TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151  CGCAGTGGAA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201  CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251  CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301  ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351  AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401  GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCATGGCA AACATGGCGC
1451  CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501  TCGCGCTACT GGCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551  GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601  ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651  CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701  CGCGTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751  CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801  CTCGAGGCGC TACAG
```

Fig. 15K Nucleotide sequence of CAB1.6i gene

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC (183)

H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)

H3CDR (373) GGGCTCCCGCTCGGGGCCATTTACAACGACTAC (405)

L1CDR (553) AGTGCCAGCTCAGCTGTATATGCCATGCAC (582)

L2CDR (628) GATACATCCAACCTGGCTTCT (648)

L3CDR (745) CAGCAAAGAGATAGTTACCCACTCACG (771)

Fig. 15L Nucleotide sequences of CAB1.7 CDRs

1	CAGGTGCAGC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAAAT	CAGGGGGCTC
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
101	TGCACTGGGT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
151	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGCTC
301	CCGCTCGGGG	CCATTTACAA	CGACTACTGG	GGCCAAGGGA	CCACGGTCAC
351	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
401	GATCAGAAAA	TGTGCTCACC	CAGTCTCCAG	CAATCGTGTC	TGCATCTCCA
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAGCTG	TATATGCCAT
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACTC	GTGATTTATG
551	ATACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
651	TGCCACTTAT	TACTGCCAGC	AAAGAGATAG	TTACCCACTC	ACGTTCGGTG
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGAAAGCCCA
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1151	CGCAGTGGAA	GCCTGGCACA	ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	ACCTGGATTA
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG	CCTGGGGCTA	TCGTGACGGT
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1451	CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG
1501	TCGCGCTACT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1701	CAGCTACGTG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG
1751	CGAATACAAG	CTATCCGAAC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1801	CTCGAGGCGC	TACAG			

Fig. 15M Nucleotide sequence of CAB1.7 gene

1	CAGGTGCAGC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAAAT	CAGGGGGCTC
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
101	TGCACTGGGT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
151	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGCTC
301	CCGCTCGGGG	CCATTTACAA	CGACTACTGG	GGCCAAGGGA	CCACGGTCAC
351	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
401	GATCAGAAAA	TGTGCTCACC	CAGTCTCCAG	CAATCGTGTC	TGCATCTCCA
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAGCTG	TATATGCCAT
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACTC	GTGATTTATG
551	ATACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
651	TGCCACTTAT	TACTGCCAGC	AAAGAGATAG	TTACCCACTC	ACGTTCGGTG
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGGCGGCCCA
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1151	CGCAGTGGAA	GCCTGGCACA	ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	ACCTGGATTA
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG	CCTGGGGCTA	TCGTGACGGT
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1451	CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG
1501	TCGCGCTACT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1701	CGCGTACGTG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG
1751	CGAATACAAG	CTATCCGAAC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1801	CTCGAGGCGC	TACAG			

Fig. 15N Nucleotide sequence of CAB1.7i gene

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC (183)

H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)

H3CDR (373) GGGACTCCGACTGGGCCGTACTACTTTGACTAC (405)

L1CDR (553) AGTGCCAGCTCAAGTGTAAGTTACATGCAC (582)

L2CDR (628) AGCACATCCAACCTGGCTTCT (648)

L3CDR (745) CAGCAAAGATCTAGTTACCCACTCACG (771)

Fig. 150 Nucleotide sequences of CAB1 CDRs

1	CAGGTGAAAC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAGGT	CAGGGACCTC
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
101	TGCACTGGTT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
151	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGACT
301	CCGACTGGGC	CGTACTACTT	TGACTACTGG	GGCCAAGGGA	CCACGGTCAC
351	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
401	GATCAGAAAA	TGTGCTCACC	CAGTCTCCAG	CAATCATGTC	TGCATCTCCA
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAAGTG	TAAGTTACAT
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACTC	TGGATTTATA
551	GCACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
651	TGCCACTTAT	TACTGCCAGC	AAAGATCTAG	TTACCCACTC	ACGTTCGGTG
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGAAAGCCCA
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1151	CGCAGTGGAA	GCCTGGCACA	ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	ACCTGGATTA
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG	CCTGGGGCTA	TCGTGACGGT
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1451	CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG
1501	TCGCGCTACT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1701	CAGCTACGTG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG
1751	CGAATACAAG	CTATCCGAAC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1801	CTCGAGGCGC	TACAG			

Fig. 15P Nucleotide sequence of CAB1 gene

H1CDR	(26) GFNIKDSYMH (35)
H2CDR	(50) WIDPENGDTEYAPKFQ (65)
H3CDR	(99) GLPLGAIYNDY (109)
L1CDR	(159) SASSSVSYMH (168)
L2CDR	(184) DTSNLAS (190)
L3CDR	(223) QQRDSYPLT (231)

Fig. 15Q Amino acid sequences of SW149.5 CDRs

H1CDR (154) GGCTTCAACATTAAAGACTCCTATATGCAC (183)

H2CDR (226) TGGATTGATCCTGAGAATGGTGATACTGAATATGCCCCGAAGTTCCAG (273)

H3CDR (373) GGGCTCCCGCTCGGGGCCATTTACAACGACTAC (405)

L1CDR (553) AGTGCCAGCTCAAGTGTAAGTTACATGCAC (582)

L2CDR (628) GATACATCCAACCTGGCTTCT (648)

L3CDR (745) CAGCAAAGAGATAGTTACCCACTCACG (771)

Fig. 15R Nucleotide sequences of SW149.5 CDRs

```
   1 CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
  51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
 101 TGCACTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
 151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
 201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
 251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGCTC
 301 CCGCTCGGGG CCATTTACAA CGACTACTGG GGCCAAGGGA CCACGGTCAC
 351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
 401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
 451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAAGTG TAAGTTACAT
 501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAACTC GTGATTTATG
 551 ATACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
 601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
 651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
 701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
 751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGAAAGCCCA
 801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
 851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
 901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
 951 AGGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGAA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CAGCTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG
```

Fig. 15S Nucleotide sequence of *SW149.5* gene

```
   1 ACACCGGTGT CAGAAAAACA GCTGGCGGAG GTGGTCGCGA ATACGATTAC
  51 CCCGCTGATG AAAGCCCAGT CTGTTCCAGG CATGGCGGTG GCCGTTATTT
 101 ATCAGGGAAA ACCGCACTAT TACACATTTG GCAAGGCCGA TATCGCGGCG
 151 AATAAACCCG TTACGCCTCA GACCCTGTTC GAGCTGGGTT CTATAAGTAA
 201 AACCTTCACC GGCGTTTTAG GTGGGGATGC CATTGCTCGC GGTGAAATTT
 251 CGCTGGACGA TGCGGTGACC AGATACTGGC CACAGCTGAC GGGCAAGCAG
 301 TGGCAGGGTA TTCGTATGCT GGATCTCGCC ACCTACACCG CTGGCGGCCT
 351 GCCGCTACAG GTACCGGATG AGGTCACGGA TAACGCCTCC CTGCTGCGCT
 401 TTTATCAAAA CTGGCAGCCG CAGTGGAAGC CTGGCACAAC GCGTCTTTAC
 451 GCCAACGCCA GCATCGGTCT TTTTGGTGCG CTGGCGGTCA AACCTTCTGG
 501 CATGCCCTAT GAGCAGGCCA TGACGACGCG GGTCCTTAAG CCGCTCAAGC
 551 TGGACCATAC CTGGATTAAC GTGCCGAAAG CGGAAGAGGC GCATTACGCC
 601 TGGGGCTATC GTGACGGTAA AGCGGTGCGC GTTTCGCCGG GTATGCTGGA
 651 TGCACAAGCC TATGGCGTGA AAACCAACGT GCAGGATATG GCGAACTGGG
 701 TCATGGCAAA CATGGCGCCG GAGAACGTTG CTGATGCCTC ACTTAAGCAG
 751 GGCATCGCGC TGGCGCAGTC GCGCTACTGG CGTATCGGGT CAATGTATCA
 801 GGGTCTGGGC TGGGAGATGC TCAACTGGCC CGTGGAGGCC AACACGGTGG
 851 TCGAGACGAG TTTTGGTAAT GTAGCACTGG CGCCGTTGCC CGTGGCAGAA
 901 GTGAATCCAC CGGCTCCCCC GGTCAAAGCG TCCTGGGTCC ATAAAACGGG
 951 CTCTACTGGC GGGTTTGGCA GCTACGTGGC CTTTATTCCT GAAAAGCAGA
1001 TCGGTATTGT GATGCTCGCG AATACAAGCT ATCCGAACCC GGCACGCGTT
1051 GAGGCGGCAT ACCATATCCT CGAGGCGCTA CAG
```

Fig. 15T Nucleotide sequence of BLA gene

1	CAGGTGAAAC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAAAT	CAGGGGGCTC
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
101	TGCACTGGTT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
151	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGACT
301	CCGACTGGGC	CGTACTACTT	TGACTACTGG	GGCCAAGGGA	CCACGGTCAC
351	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
401	GATCAGAAAA	TGTGCTCACC	CAGTCTCCAG	CAATCATGTC	TGCATCTCCA
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAAGTG	TAAGTTACAT
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACTC	GTGATTTATA
551	GCACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
651	TGCCACTTAT	TACTGCCAGC	AAAGATCTAG	TTACCCACTC	ACGTTCGGTG
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGAAAGCCCA
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1151	CGCAGTGGAA	GCCTGGCACA	ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	ACCTGGATTA
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG	CCTGGGGCTA	TCGTGACGGT
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1451	CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG
1501	TCGCGCTACT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1701	CAGCTACGTG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG
1751	CGAATACAAG	CTATCCGAAC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1801	CTCGAGGCGC	TACAG			

Fig. 15U Nucleotide sequence of CAB1.1 gene

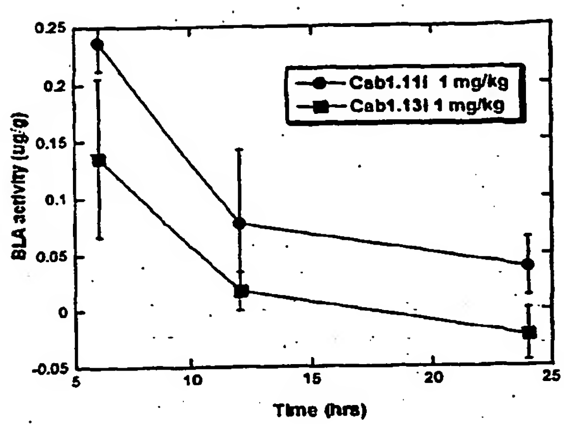

Cab1.11i 1 mg/kg
Cab1.13i 1 mg/kg
BLA activity (ug/g)
Time (hrs)
0.25
0.2
0.15
0.1
0.05
0
-0.05
5
10
15
20
25

Figure 16

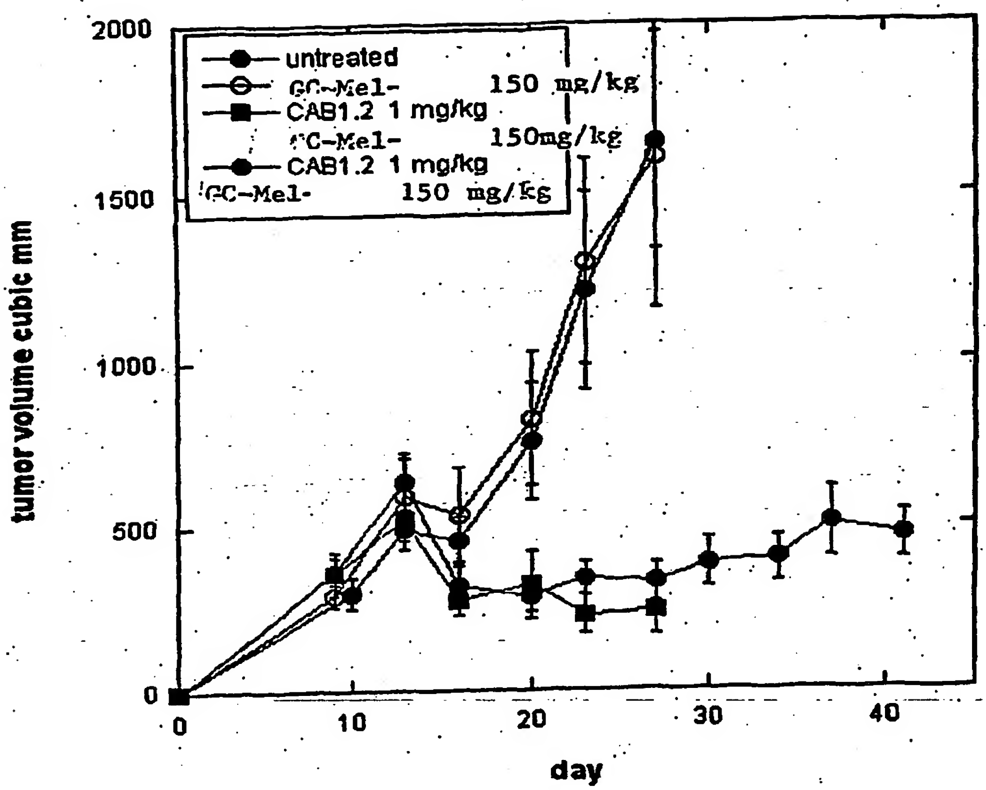

untreated
GC-Mel- 150 mg/kg
CAB1.2 1 mg/kg
GC-Mel- 150mg/kg
CAB1.2 1 mg/kg
GC-Mel- 150 mg/kg
tumor volume cubic mm
2000
1500
1000
500
0
0
10
20
30
40
day

Figure 17

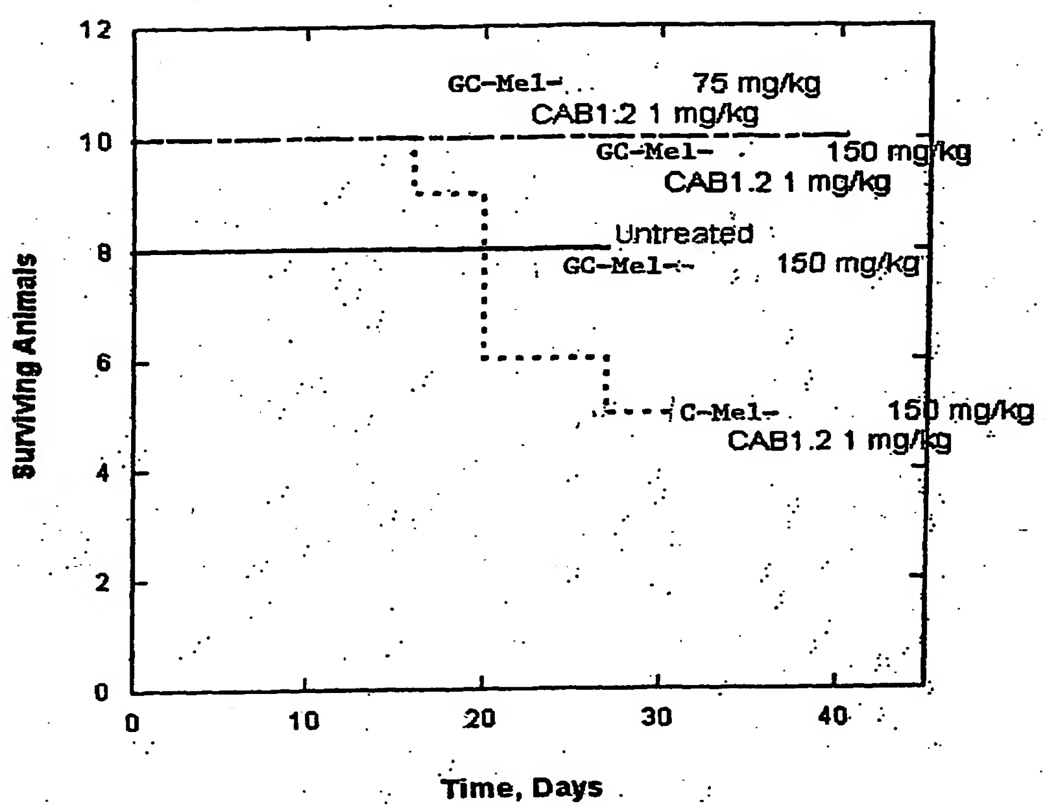

12
10
8
6
4
2
0
Surviving Animals
0
10
20
30
40
Time, Days
GC-Mel- 75 mg/kg
CAB1.2 1 mg/kg
GC-Mel- 150 mg/kg
CAB1.2 1 mg/kg
Untreated
GC-Mel- 150 mg/kg
C-Mel- 150 mg/kg
CAB1.2 1 mg/kg

Figure 18

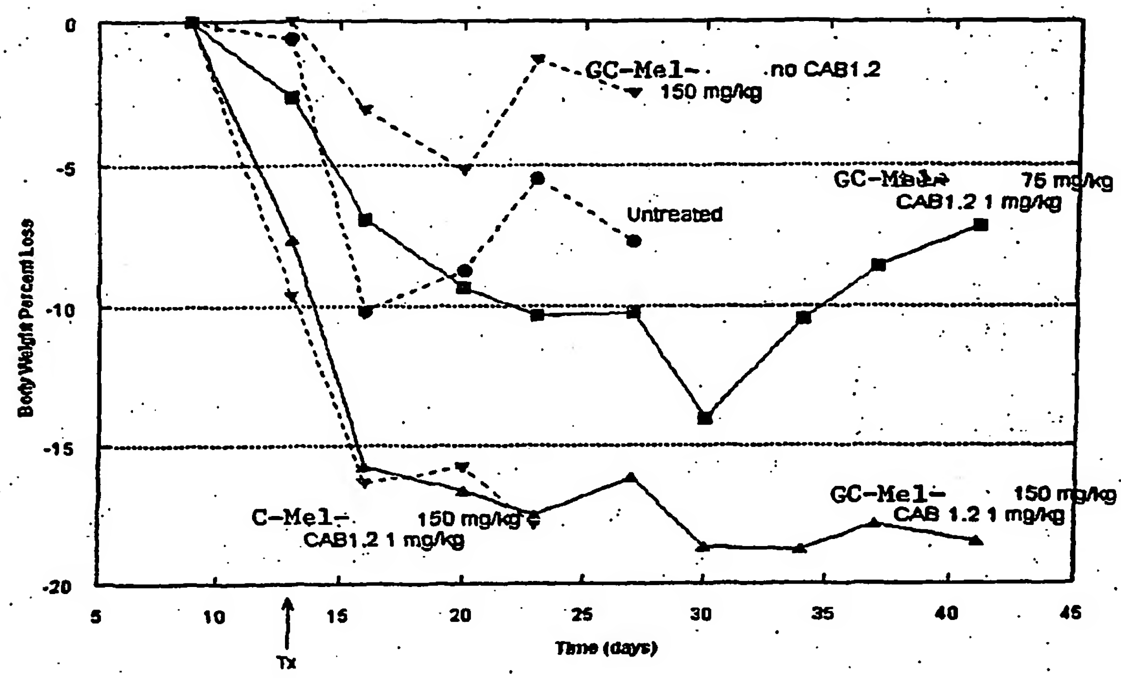

GC-Mel- no CAB1.2
150 mg/kg
GC-Mel- 75 mg/kg
CAB1.2 1 mg/kg
Untreated
GC-Mel- 150 mg/kg
CAB 1.2 1 mg/kg
C-Mel- 150 mg/kg
CAB1.2 1 mg/kg
Body Weight Percent Loss
0
-5
-10
-15
-20
5
10
15
20
25
30
35
40
45
Time (days)
Tx

Figure 19

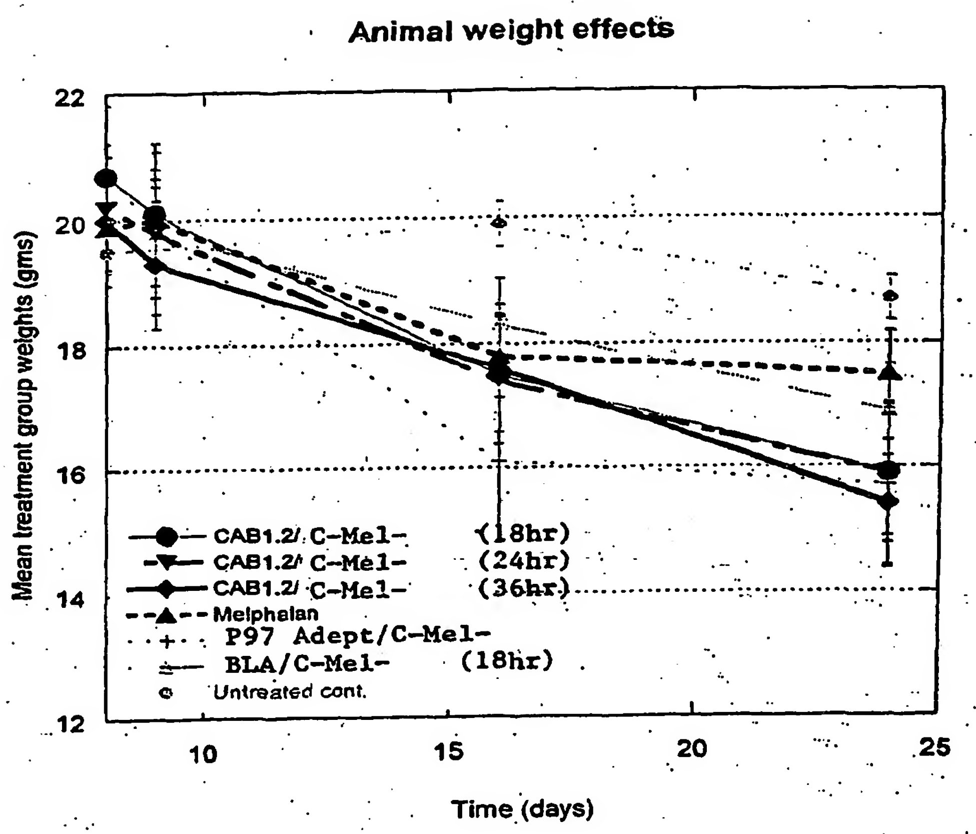

Animal weight effects
Mean treatment group weights (gms)
22
20
18
16
14
12
10
15
20
25
Time (days)
CAB1.2/ C-Mel- (18hr)
CAB1.2/ C-Mel- (24hr)
CAB1.2/ C-Mel- (36hr)
Melphalan
P97 Adept/C-Mel-
BLA/C-Mel- (18hr)
Untreated cont.

Figure 20

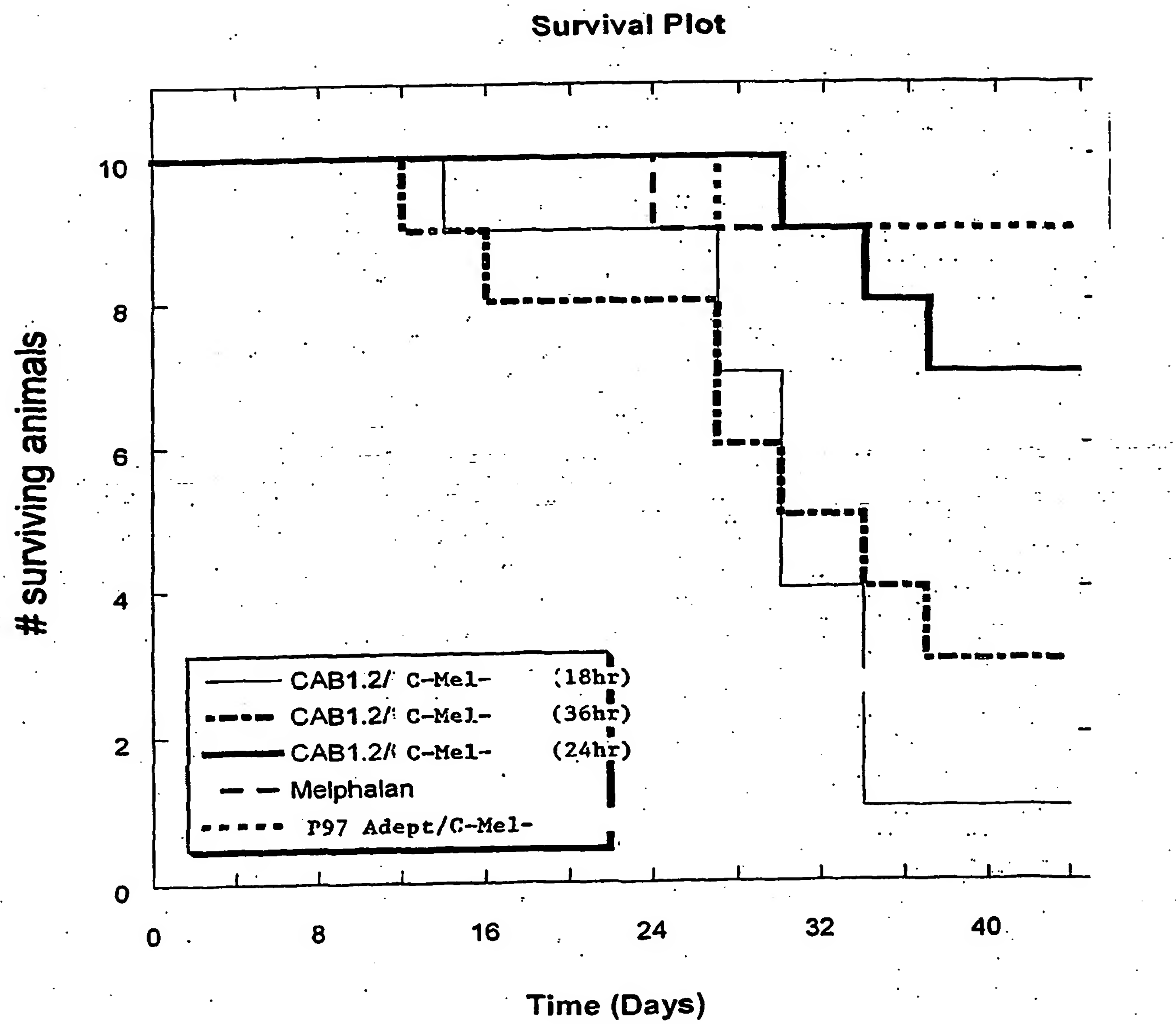
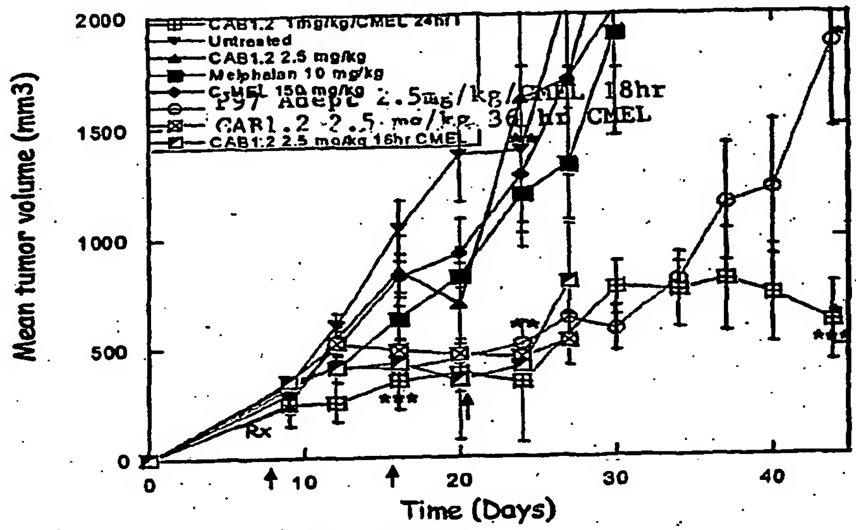

Survival Plot
surviving animals
10
8
6
4
2
0
0
8
16
24
32
40
Time (Days)
CAB1.2/ C-Mel- (18hr)
CAB1.2/ C-Mel- (36hr)
CAB1.2/ C-Mel- (24hr)
Melphalan
P97 Adept/C-Mel-

Figure 21

CAB1 Proof of Principle – Efficacy#



*p<0.05 sgn17 vs CAB1.2(24h)
**p<0.05 untreated vs CAB1.2(18,24,36h)
***GC observed in 2 animals: 1 Day 16; 1 Day 44

Figure 11

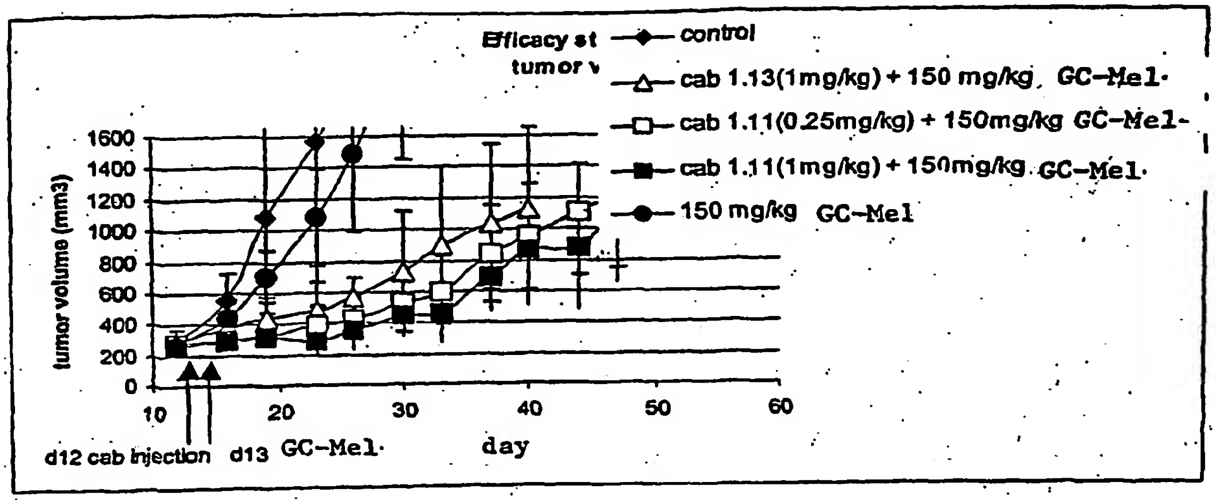

Efficacy st
tumor v
control
cab 1.13(1mg/kg) + 150 mg/kg GC-Mel
cab 1.11(0.25mg/kg) + 150mg/kg GC-Mel
cab 1.11(1mg/kg) + 150mg/kg GC-Mel
150 mg/kg GC-Mel
tumor volume (mm3)
1600
1400
1200
1000
800
600
400
200
0
10
20
30
40
50
60
day
d12 cab injection
d13 GC-Mel

Figure 23

```
  1 QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
 51 IDPENGDTEY APKFQGKATF TTDTSSNTAY LQLSSLTSED TAVYYCNEGT
101 PTGPYYFDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151 GEKVTITCSA SSSVSYMHWF QQKPGTSPKL VIYSTSNLAS GVPARFSGSG
201 SGTSYSLTIS RMEAEDAATY YCQQRSSYPL TFGAGTKLEL KRAATPVSEK
251 QLAEVVANTI TPLMAAQSVP GMAVAVIYQG KPHYYTFGKA DIAANKPVTP
301 QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351 LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401 LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451 KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501 SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551 PVKASWVHKT GSTGGFGAYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601 LEALQ
```

Figure 24A

1	CAGGTGCAGC	TGCAGCAGTC	TGGGGCAGAA	CTTGTGAAAT	CAGGGGGCTC
51	AGTCAAGTTG	TCCTGCACAG	CTTCTGGCTT	CAACATTAAA	GACTCCTATA
101	TGCACTGGGT	GAGGCAGGGG	CCTGAACAGG	GCCTGGAGTG	GATTGGATGG
151	ATTGATCCTG	AGAATGGTGA	TACTGAATAT	GCCCCGAAGT	TCCAGGGCAA
201	GGCCACTTTT	ACTACAGACA	CATCCTCCAA	CACAGCCTAC	CTGCAGCTCA
251	GCAGCCTGAC	ATCTGAGGAC	ACTGCCGTCT	ATTATTGTAA	TGAGGGGACT
301	CCGACTGGGC	CGTACTACTT	TGACTACTGG	GGCCAAGGGA	CCACGGTCAC
351	CGTCTCCTCA	GGTGGAGGCG	GTTCAGGCGG	AGGTGGCTCT	GGCGGTGGCG
401	GATCAGAAAA	TGTGCTCACC	CAGTCTCCAG	CAATCGTGTC	TGCATCTCCA
451	GGGGAGAAGG	TCACCATAAC	CTGCAGTGCC	AGCTCAAGTG	TAAGTTACAT
501	GCACTGGTTC	CAGCAGAAGC	CAGGCACTTC	TCCCAAACTC	GTGATTTATA
551	GCACATCCAA	CCTGGCTTCT	GGAGTCCCTG	CTCGCTTCAG	TGGCAGTGGA
601	TCTGGGACCT	CTTACTCTCT	CACAATCAGC	CGAATGGAGG	CTGAAGATGC
651	TGCCACTTAT	TACTGCCAGC	AAAGATCTAG	TTACCCACTC	ACGTTCGGTG
701	CTGGCACCAA	GCTGGAGCTG	AAACGGGCGG	CCACACCGGT	GTCAGAAAAA
751	CAGCTGGCGG	AGGTGGTCGC	GAATACGATT	ACCCCGCTGA	TGGCGGCCCA
801	GTCTGTTCCA	GGCATGGCGG	TGGCCGTTAT	TTATCAGGGA	AAACCGCACT
851	ATTACACATT	TGGCAAGGCC	GATATCGCGG	CGAATAAACC	CGTTACGCCT
901	CAGACCCTGT	TCGAGCTGGG	TTCTATAAGT	AAAACCTTCA	CCGGCGTTTT
951	AGGTGGGGAT	GCCATTGCTC	GCGGTGAAAT	TTCGCTGGAC	GATGCGGTGA
1001	CCAGATACTG	GCCACAGCTG	ACGGGCAAGC	AGTGGCAGGG	TATTCGTATG
1051	CTGGATCTCG	CCACCTACAC	CGCTGGCGGC	CTGCCGCTAC	AGGTACCGGA
1101	TGAGGTCACG	GATAACGCCT	CCCTGCTGCG	CTTTTATCAA	AACTGGCAGC
1151	CGCAGTGGAA	GCCTGGCACA	ACGCGTCTTT	ACGCCAACGC	CAGCATCGGT
1201	CTTTTTGGTG	CGCTGGCGGT	CAAACCTTCT	GGCATGCCCT	ATGAGCAGGC
1251	CATGACGACG	CGGGTCCTTA	AGCCGCTCAA	GCTGGACCAT	ACCTGGATTA
1301	ACGTGCCGAA	AGCGGAAGAG	GCGCATTACG	CCTGGGGCTA	TCGTGACGGT
1351	AAAGCGGTGC	GCGTTTCGCC	GGGTATGCTG	GATGCACAAG	CCTATGGCGT
1401	GAAAACCAAC	GTGCAGGATA	TGGCGAACTG	GGTCATGGCA	AACATGGCGC
1451	CGGAGAACGT	TGCTGATGCC	TCACTTAAGC	AGGGCATCGC	GCTGGCGCAG
1501	TCGCGCTACT	GGCGTATCGG	GTCAATGTAT	CAGGGTCTGG	GCTGGGAGAT
1551	GCTCAACTGG	CCCGTGGAGG	CCAACACGGT	GGTCGAGACG	AGTTTTGGTA
1601	ATGTAGCACT	GGCGCCGTTG	CCCGTGGCAG	AAGTGAATCC	ACCGGCTCCC
1651	CCGGTCAAAG	CGTCCTGGGT	CCATAAAACG	GGCTCTACTG	GCGGGTTTGG
1701	CGCGTACGTG	GCCTTTATTC	CTGAAAAGCA	GATCGGTATT	GTGATGCTCG
1751	CGAATACAAG	CTATCCGAAC	CCGGCACGCG	TTGAGGCGGC	ATACCATATC
1801	CTCGAGGCGC	TACAG			

Figure 24B

```
  1  QVQLQQSGAE LVKSGGSVKL SCTASGFNIK DSYMHWVRQG PEQGLEWIGW
 51  IDPENGDTEY APKFQGKATF TTDTSSNTAY LQLSSLTSED TAVYYCNEGL
101  PLGAIYNDYW GQGTTVTVSS GGGGSGGGGS GGGGSENVLT QSPAIVSASP
151  GEKVTITCSA SSAVYAMHWF QQKPGTSPKL VIYSTSNLAS GVPARFSGSG
201  SGTSYSLTIS RMEAEDAATY YCQQRDSYPL TFGAGTKLEL KRAATPVSEK
251  QLAEVVANTI TPLMAAQSVP GMAVAVIYQG KPHYYTFGKA DIAANKPVTP
301  QTLFELGSIS KTFTGVLGGD AIARGEISLD DAVTRYWPQL TGKQWQGIRM
351  LDLATYTAGG LPLQVPDEVT DNASLLRFYQ NWQPQWKPGT TRLYANASIG
401  LFGALAVKPS GMPYEQAMTT RVLKPLKLDH TWINVPKAEE AHYAWGYRDG
451  KAVRVSPGML DAQAYGVKTN VQDMANWVMA NMAPENVADA SLKQGIALAQ
501  SRYWRIGSMY QGLGWEMLNW PVEANTVVET SFGNVALAPL PVAEVNPPAP
551  PVKASWVHKT GSTGGFGAYV AFIPEKQIGI VMLANTSYPN PARVEAAYHI
601  LEALQ
```

Figure 24C

1 CAGGTGCAGC TGCAGCAGTC TGGGGCAGAA CTTGTGAAAT CAGGGGGCTC
51 AGTCAAGTTG TCCTGCACAG CTTCTGGCTT CAACATTAAA GACTCCTATA
101 TGCACTGGGT GAGGCAGGGG CCTGAACAGG GCCTGGAGTG GATTGGATGG
151 ATTGATCCTG AGAATGGTGA TACTGAATAT GCCCCGAAGT TCCAGGGCAA
201 GGCCACTTTT ACTACAGACA CATCCTCCAA CACAGCCTAC CTGCAGCTCA
251 GCAGCCTGAC ATCTGAGGAC ACTGCCGTCT ATTATTGTAA TGAGGGGCTC
301 CCGCTCGGGG CCATTTACAA CGACTACTGG GGCCAAGGGA CCACGGTCAC
351 CGTCTCCTCA GGTGGAGGCG GTTCAGGCGG AGGTGGCTCT GGCGGTGGCG
401 GATCAGAAAA TGTGCTCACC CAGTCTCCAG CAATCGTGTC TGCATCTCCA
451 GGGGAGAAGG TCACCATAAC CTGCAGTGCC AGCTCAGCTG TATATGCCAT
501 GCACTGGTTC CAGCAGAAGC CAGGCACTTC TCCCAAACTC GTGATTTATA
551 GCACATCCAA CCTGGCTTCT GGAGTCCCTG CTCGCTTCAG TGGCAGTGGA
601 TCTGGGACCT CTTACTCTCT CACAATCAGC CGAATGGAGG CTGAAGATGC
651 TGCCACTTAT TACTGCCAGC AAAGAGATAG TTACCCACTC ACGTTCGGTG
701 CTGGCACCAA GCTGGAGCTG AAACGGGCGG CCACACCGGT GTCAGAAAAA
751 CAGCTGGCGG AGGTGGTCGC GAATACGATT ACCCCGCTGA TGGCGGCCCA
801 GTCTGTTCCA GGCATGGCGG TGGCCGTTAT TTATCAGGGA AAACCGCACT
851 ATTACACATT TGGCAAGGCC GATATCGCGG CGAATAAACC CGTTACGCCT
901 CAGACCCTGT TCGAGCTGGG TTCTATAAGT AAAACCTTCA CCGGCGTTTT
951 GGTGGGGAT GCCATTGCTC GCGGTGAAAT TTCGCTGGAC GATGCGGTGA
1001 CCAGATACTG GCCACAGCTG ACGGGCAAGC AGTGGCAGGG TATTCGTATG
1051 CTGGATCTCG CCACCTACAC CGCTGGCGGC CTGCCGCTAC AGGTACCGGA
1101 TGAGGTCACG GATAACGCCT CCCTGCTGCG CTTTTATCAA AACTGGCAGC
1151 CGCAGTGGAA GCCTGGCACA ACGCGTCTTT ACGCCAACGC CAGCATCGGT
1201 CTTTTTGGTG CGCTGGCGGT CAAACCTTCT GGCATGCCCT ATGAGCAGGC
1251 CATGACGACG CGGGTCCTTA AGCCGCTCAA GCTGGACCAT ACCTGGATTA
1301 ACGTGCCGAA AGCGGAAGAG GCGCATTACG CCTGGGGCTA TCGTGACGGT
1351 AAAGCGGTGC GCGTTTCGCC GGGTATGCTG GATGCACAAG CCTATGGCGT
1401 GAAAACCAAC GTGCAGGATA TGGCGAACTG GGTCATGGCA AACATGGCGC
1451 CGGAGAACGT TGCTGATGCC TCACTTAAGC AGGGCATCGC GCTGGCGCAG
1501 TCGCGCTACT GGCGTATCGG GTCAATGTAT CAGGGTCTGG GCTGGGAGAT
1551 GCTCAACTGG CCCGTGGAGG CCAACACGGT GGTCGAGACG AGTTTTGGTA
1601 ATGTAGCACT GGCGCCGTTG CCCGTGGCAG AAGTGAATCC ACCGGCTCCC
1651 CCGGTCAAAG CGTCCTGGGT CCATAAAACG GGCTCTACTG GCGGGTTTGG
1701 CGCGTACGTG GCCTTTATTC CTGAAAAGCA GATCGGTATT GTGATGCTCG
1751 CGAATACAAG CTATCCGAAC CCGGCACGCG TTGAGGCGGC ATACCATATC
1801 CTCGAGGCGC TACAG

Figure 24D

```
1    DIVLTQSPAS LSVSLGQRAT MSCRAGESVD IFGVGFLHWY QQKPGQPPKL
51   LIYRASNLES GIPVRFSGTG SGTDFTLIID PVEADDVATY YCQQTNEDPY
101  TFGGGTKLEI KGGGGSGGGG SGGGGSGGGG SGGGGSGGGG SEVQLQQSGA
151  ELVEPGASVK LSCTASGFNI KDTYMHWVKQ RPEQGLEWIG RIDPANGNSK
201  YVPKFQGKAT ITADTSSNTA YLQLTSLTSE DTAVYYCAPF GYYVSDYAMA
251  YWGQGTSVTV SSTPVSEKQL AEVVANTITP LMAAQSVPGM AVAVIYQGKP
301  HYYTFGKADI AANKPVTPQT LFELGSISKT FTGVLGGDAI ARGEISLDDA
351  VTRYWPQLTG KQWQGIRMLD LATYTAGGLP LQVPDEVTDN ASLLRFYQNW
401  QPQWKPGTTR LYANASIGLF GALAVKPSGM PYEQAMTTRV LKPLKLDHTW
451  INVPKAEEAH YAWGYRDGKA VRVSPGMLDA QAYGVKTNVQ DMANWVMANM
501  APENVADASL KQGIALAQSR YWRIGSMYQG LGWEMLNWPV EANTVVETSF
551  GNVALAPLPV AEVNPPAPPV KASWVHKTGS TGGFGAYVAF IPEKQIGIVM
601  LANTSYPNPA RVEAAYHILE ALQ
```

Figure 25A

```
   1  GACATCGTCC TGACCCAGAG CCCGGCAAGC CTGTCTGTTT CCCTGGGCCA
  51  GCGTGCCACT ATGTCCTGCA GAGCGGGTGA GTCTGTTGAC ATTTTCGGTG
 101  TCGGTTTTCT GCACTGGTAC CAACAGAAAC CGGGTCAGCC GCCAAAACTG
 151  CTGATCTATC GTGCTTCTAA CCTGGAGTCC GGCATCCCGG TACGTTTCTC
 201  CGGTACTGGC TCTGGTACTG ATTTTACCCT GATTATCGAC CCGGTGGAAG
 251  CAGACGATGT TGCCACCTAC TATTGCCAGC AGACCAACGA GGATCCGTAC
 301  ACCTTCGGTG GCGGTACTAA ACTGGAGATC AAAGGCGGTG GTGGTTCTGG
 351  TGGTGGTGGT AGCGGTGGCG GTGGTAGCGG TGGCGGTGGC AGCGGTGGTG
 401  GTGGCTCTGG TGGCGGTGGC TCTGAAGTGC AGCTGCAGCA GTCCGGTGCG
 451  GAGCTCGTTG AACCGGGCGC TTCTGTGAAA CTGTCTTGCA CTGCATCTGG
 501  TTTCAACATT AAGGACACCT ACATGCACTG GGTGAAACAA CGCCCGGAAC
 551  AGGGTCTGGA GTGGATCGGT CGCATCGATC CGGCTAACGG TAACAGCAAA
 601  TACGTGCCAA AATTCCAGGG TAAAGCAACC ATCACTGCTG ATACCTCCTC
 651  TAACACTGCT TACCTGCAGC TGACTTCCCT GACTAGCGAA GACACCGCGG
 701  TTTATTACTG CGCTCCGTTC GGCTACTATG TCAGCGATTA CGCAATGGCC
 751  TACTGGGGTC AGGGCACCTC TGTTACCGTT TCTAGCACAC CGGTGTCAGA
 801  AAAACAGCTG GCGGAGGTGG TCGCGAATAC GATTACCCCG CTGATGGCGG
 851  CCCAGTCTGT TCCAGGCATG GCGGTGGCCG TTATTTATCA GGGAAAACCG
 901  CACTATTACA CATTTGGCAA GGCCGATATC GCGGCGAATA AACCCGTTAC
 951  GCCTCAGACC CTGTTCGAGC TGGGTTCTAT AAGTAAAACC TTCACCGGCG
1001  TTTTAGGTGG GGATGCCATT GCTCGCGGTG AAATTTCGCT GGACGATGCG
1051  GTGACCAGAT ACTGGCCACA GCTGACGGGC AAGCAGTGGC AGGGTATTCG
1101  TATGCTGGAT CTCGCCACCT ACACCGCTGG CGGCCTGCCG CTACAGGTAC
1151  CGGATGAGGT CACGGATAAC GCCTCCCTGC TGCGCTTTTA TCAAAACTGG
1201  CAGCCGCAGT GGAAGCCTGG CACAACGCGT CTTTACGCCA ACGCCAGCAT
1251  CGGTCTTTTT GGTGCGCTGG CGGTCAAACC TTCTGGCATG CCCTATGAGC
1301  AGGCCATGAC GACGCGGGTC CTTAAGCCGC TCAAGCTGGA CCATACCTGG
1351  ATTAACGTGC CGAAAGCGGA AGAGGCGCAT TACGCCTGGG GCTATCGTGA
1401  CGGTAAAGCG GTGCGCGTTT CGCCGGGTAT GCTGGATGCA CAAGCCTATG
1451  GCGTGAAAAC CAACGTGCAG GATATGGCGA ACTGGGTCAT GGCAAACATG
1501  GCGCCGGAGA ACGTTGCTGA TGCCTCACTT AAGCAGGGCA TCGCGCTGGC
1551  GCAGTCGCGC TACTGGCGTA TCGGGTCAAT GTATCAGGGT CTGGGCTGGG
1601  AGATGCTCAA CTGGCCCGTG GAGGCCAACA CGGTGGTCGA GACGAGTTTT
1651  GGTAATGTAG CACTGGCGCC GTTGCCCGTG GCAGAAGTGA ATCCACCGGC
1701  TCCCCCGGTC AAAGCGTCCT GGGTCCATAA AACGGGCTCT ACTGGCGGGT
1751  TTGGCGCGTA CGTGGCCTTT ATTCCTGAAA AGCAGATCGG TATTGTGATG
1801  CTCGCGAATA CAAGCTATCC GAACCCGGCA CGCGTTGAGG CGGCATACCA
1851  TATCCTCGAG GCGCTACAG
```

Figure 25B

Case ID	ASM	Sample ID	Sample Pathology
CI0000000255	DF5	FR00005C7B	Adenocarcinoma of lung
CI0000005496	FF5	FR5B337147	Adenocarcinoma of lung
CI0000011577	FF1	FR5B34059F	Adenocarcinoma of lung
CI7000000241	AF4	FR00033A78	Adenocarcinoma of lung
CI0000007518	AF5	FR0001FD15	Carcinoma of lung, squamous cell
CI0000008475	HF4	FR65EE0784	Adenocarcinoma of colon, metastatic
CI0000015252	FF2	FR5B342166	Adenocarcinoma of colon

Figure 26

26_A	26_B	26_C	26_D	26_E
26_F	26_G	26_H	26_I	26_J

FIGURE 26

FIG. 26-A

Case Diagnosis	Tissue of Origin/Site of Finding	H/E		Anti-H
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	4X	20X	Immunoger 4x
Adenocarcinoma of lung Grade: AJCC G3: Poorly differentiated Stage: IIIB	Lung/Lung	4X	20X	
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung	4X	20X	
Adenocarcinoma of lung Grade: AJCC G2: Moderately differentiated Stage: IIIA	Lung/Lung	4X	20X	
Carcinoma of lung, squamous cell Grade: AJCC G3: Poorly differentiated Stage: IIIA	Lung/Lung	4X	20X	
Adenocarcinoma of colon, metastatic Grade: Not Reported Stage: IV	Colon/Liver	4X	20X	Immunc Fibr No 4x
Adenocarcinoma of colon Grade: AJCC G3: Poorly differentiated Stage: IIIB	Cecum/Cecum	4X	20X	

FIG. 26-B

luman Cytokeratin AE1/AE3	CAB/GCR3708 (0.2ug/ml)	CAB/GCR55
ncity: Tumor(100%, Variable to 3+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 20x SF00029758	Immunogencity: Tumor(100%, Variable to 3+ Cyto) Mixed inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x SF00029756	Immunogencity: Tumor(1(Mixed inflammatory cel Necrosis(Variа Specifici 4x SF000
	Immunogencity: Tumor(15%, Variable to 3+ Cyto) Intra-alveolar macrophages(Variable to 2+ Cyto) Mixed inflammatory cells(Variable to 2+ Cyto) Specificity: High 4x 20x SF0002975B	Immunogencity: Tumor(4 Intra-alveolar macrophag Mixed inflammatory cel Specifici 4x SF000
	Immunogencity: Tumor(100%, 2+ Cyto) Cellular stroma(1+ Cyto) Chronic Inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x SF0002977F	Immunogencity: Tur Cellular stroi Chronic inflammatory ce Specifici 4x SF000
	Immunogencity: Tumor(75%, Variable to 3+ Cyto) Cellular Stroma(Variable to 2+ Cyto) Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable to 2+ Cyto) Specificity: High 4x 20x SF0002978B	Immunogencity: Tumor(6 Cellular Stroma(V Necrosis(Vari Intra-alveolar macropha Specifici 4x SF000
	Immunogencity: Tumor(100%, 3+ Cyto) Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x SF0002975F	Immunogencity: Tur Fibrotic stroi Necrosis(Vari Specifici 4x SF000
ogencity: Tumor(98%, Variable to 3+ Mem,Variable to 3+ Cyto) rotic stroma(Variable to 1+ Cyto) rmal liver parenchyma(2+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 20x SF0002976A	Immunogencity: Tumor(95%, Variable to 3+ Mem,Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Normal liver parenchyma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x SF00029768 Normal liver parenchyma shows positive staining (1+)	Immunogencity: Tum Mem,Variabl Fibrotic stroma(V Normal liver pare Necrosis(Vari Specifici 4x SF000
	Immunogencity: Tumor(85%, Variable to 3+ Mem,Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029783	Immunogencity: Tum Mem,Variabl Cellular stroi Normal muscle(V Specifici 4x SF000

FIG. 26-C

17 (0.2ug/ml)	CAB/GCR6798 (0.2ug/ml)	CAB/GCR8886 (0.196ug/
00%, Variable to 3+ Cyto) lls(Variable to 3+ Cyto) able to 2+ EC) ity: High 20x '29757	Immunogencity: Tumor(100%, Variable to 3+ Cyto) Mixed inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x SF00029753	Immunogencity: Tumor(100%, Variable Mixed inflammatory cells(Variable to Specificity: High 4x 20x SF00029754
10%, Variable to 3+ Cyto) ges(Variable to 2+ Cyto) lls(Variable to 2+ Cyto) ity: High 20x 2975C	Immunogencity: Tumor(10%, Variable to 2+ Cyto) Intra-alveolar macrophages(Variable to 2+ Cyto) Mixed inflammatory cells(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029759	Immunogencity: Tumor(10%, Variable t Intra-alveolar macrophages(Variable tc Mixed inflammatory cells(Variable to Specificity: High 4x 20x SF0002975A
mor(100%, 2+ Cyto) ma(1+ Cyto) ells(Variable to 1+ Cyto) ity: High 20x '29780	Immunogencity: Tumor(100%, 2+ Cyto) Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to 1+ Cyto) Specificity: High 4x 20x SF0002977D	Immunogencity: Tumor(100%, 2+ Cellular stroma(1+ Cyto) Chronic inflammatory cells(Variable to Specificity: High 4x 20x SF0002977E
5%, Variable to 3+ Cyto) ariable to 2+ Cyto) able to 2+ EC) ges(Variable to 2+ Cyto) ity: High 20x 2978C	Immunogencity: Tumor(75%, Variable to 3+ Cyto) Cellular Stroma(Variable to 2+ Cyto) Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029789	Immunogencity: Tumor(75%, Variable t Cellular Stroma(Variable to 2+ C Necrosis(Variable to 2+ EC) Intra-alveolar macrophages(Variable tc Specificity: High 4x 20x SF0002978A
mor(100%, 3+ Cyto) ma(1+ Cyto) able to 3+ EC) ity: High 20x '29760	Immunogencity: Tumor(100%, 3+ Cyto) Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x SF0002975D	Immunogencity: Tumor(100%, 3+ Fibrotic stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x SF0002975E
r(98%, Variable to 3+ e to 3+ Cyto) ariable to 1+ Cyto) nchyma(2+ Cyto) able to 3+ EC) ity: High 20x '29769	Immunogencity: Tumor(95%, Variable to 3+ Mem,Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Normal liver parenchyma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x SF00029765 Normal liver parenchyma shows positive staining (1+)	Immunogencity: Tumor(95%, Variab Mem,Variable to 3+ Cyto) Fibrotic stroma(Variable to 1+ C Normal liver parenchyma(1+ Cy Necrosis(Variable to 3+ EC) Specificity: High 4x 20x SF00029766 Normal liver parenchyma shows positive s
or(85%, Variable to 3+ e to 3+ Cyto) ma(1+ Cyto) ariable to 2+ Cyto) ity: High 20x '29784	Immunogencity: Tumor(95%, Variable to 3+ Mem,Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029781	Immunogencity: Tumor(95%, Variab Mem,Variable to 3+ Cyto) Cellular stroma(1+ Cyto) Normal muscle(Variable to 2+ C Specificity: High 4x 20x SF00029782

FIG. 26-D

ml)	No Antibody control (Prediluted)
to 3+ Cyto) 1+ Cyto)	Immunogencity: N/A Specificity: Unknown SF00029755
to 2+ Cyto) 2+ Cyto) 2+ Cyto)	
Cyto) 1+ Cyto)	
to 3+ Cyto) yto) 2+ Cyto)	
Cyto)	
le to 3+ yto) to) taining (1+)	Immunogencity: N/A Specificity: Unknown SF00029767
le to 3+ yto)	

FIG. 26-E

CI0000017970	HF1	FR65EE7B3D	Adenocarcinoma of colon
CI0000010013	AF2	FR00028F2E	Adenocarcinoma of pancreas, metastatic
CI0000009651	AF1	FR0002B111	Adenocarcinoma of pancreas, ductal
CI0000008690	CF4	FR00027B0E	Adenocarcinoma of pancreas, ductal
CI0000007678	AF3	FR0002575B	Adenocarcinoma of pancreas, ductal
CI0000009736	AF2	FR0002BAB4	Adenocarcinoma of pancreas, ductal

FIG. 26-F

Adenocarcinoma of colon Grade: AJCC G2: Moderately differentiated Stage: IIIC	Colon/Colon	4X	20X	
Adenocarcinoma of pancreas, metastatic Grade: Not Reported Stage: IV	Pancreas/Omentum	4X	20X	Immu Fibroa 4x
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	4X	20X	
Adenocarcinoma of pancreas, ductal Grade: AJCC G1: Well differentiated Stage: IIA	Pancreas/Pancreas	4X	20X	
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: III	Pancreas/Pancreas	4X	20X	
Adenocarcinoma of pancreas, ductal Grade: AJCC G2: Moderately differentiated Stage: IIB	Pancreas/Pancreas	4X	20X	

FIG. 26-G

Immunogencity: Tumor(100%, 3+ Cyto)
Cellular stroma(1+ Cyto)
Necrosis(Variable to 3+ EC)
Specificity: High
4x 20x
SF00029787

Immunogencity: Tu
Cellular stro
Necrosis(Vari
Specifici
4x
SF000

ınogencity: Tumor(100%, 3+ Cyto)
adipose tissue(Variable to 1+ Cyto)
Specificity: High
20x
SF0002977C

Immunogencity: Tumor(100%, 3+ Cyto)
Fibroadipose tissue(Variable to 2+ Cyto)
Specificity: High
4x 20x
SF0002977A

Immunogencity: Tur
Fibroadipose tissue(
Specifici
4x
SF000.

Immunogencity: Tumor(100%, 3+ Cyto)
Desmoplastic stroma(Variable to 2+ Cyto)
Specificity: High
4x 20x
SF00029771

Immunogencity: Tur
Desmoplastic stroma
Specifici
4x
SF000

Immunogencity: Tumor(100%, 3+ Cyto)
Myxoid stroma(Variable to 2+ Cyto)
Specificity: High
4x 20x
SF0002976D

Immunogencity: Tur
Myxoid stroma(Va
Specifici
4x
SF000.

Immunogencity: Tumor(85%, Variable to 3+ Cyto)
Cellular stroma(Variable to 1+ Cyto)
Chronic pancreatitis(Variable to 1+ Cyto)
Specificity: High
4x 20x
SF00029763

Immunogencity: Tumor(8
Cellular stroma(V
Chronic pancreatitis(
Specifici
4x
SF000

Immunogencity: Tumor(100%, 3+ Cyto)
Chronic pancreatitis(Variable to 2+ Cyto)
Fibrotic stroma(Variable to 2+ Cyto)
Specificity: High
4x 20x
SF00029775

Immunogencity: Tur
Chronic pancreatitis(
Fibrotic stroma(V
Specifici
4x
SF000

FIG. 26-H

nor(100%, 3+ Cyto) ma(1+ Cyto) able to 3+ EC) ity: High 20x 29788	Immunogencity: Tumor(100%, 3+ Cyto) Cellular stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x SF00029785	Immunogencity: Tumor(100%, 3+ Cellular stroma(1+ Cyto) Necrosis(Variable to 3+ EC) Specificity: High 4x 20x SF00029786
nor(100%, 3+ Cyto) Variable to 2+ Cyto) ity: High 20x 2977B	Immunogencity: Tumor(100%, 3+ Cyto) Fibroadipose tissue(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029777	Immunogencity: Tumor(100%, 3+ Fibroadipose tissue(Variable to 2+ Specificity: High 4x 20x SF00029778
nor(100%, 3+ Cyto) (Variable to 2+ Cyto) ity: High 20x 29772	Immunogencity: Tumor(100%, 3+ Cyto) Desmoplastic stroma(Variable to 2+ Cyto) Specificity: High 4x 20x SF00029770	Immunogencity: Tumor(100%, 3+ Desmoplastic stroma(Variable to 2 Specificity: High 4x 20x SF0002976F
nor(100%, 3+ Cyto) ariable to 2+ Cyto) ity: High 20x 2976E	Immunogencity: Tumor(100%, 3+ Cyto) Myxoid stroma(Variable to 2+ Cyto) Specificity: High 4x 20x SF0002976B	Immunogencity: Tumor(100%, 3+ Myxoid stroma(Variable to 2+ C Specificity: High 4x 20x SF0002976C
5%, Variable to 3+ Cyto) ariable to 1+ Cyto) (Variable to 1+ Cyto) ity: High 20x 29764	Immunogencity: Tumor(85%, Variable to 3+ Cyto) Cellular stroma(Variable to 1+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Specificity: High 4x 20x SF00029761	Immunogencity: Tumor(85%, Variable t Cellular stroma(Variable to 1+ C Chronic pancreatitis(Variable to 1+ Specificity: High 4x 20x SF00029762
nor(100%, 3+ Cyto) (Variable to 2+ Cyto) ariable to 2+ Cyto) ity: High 20x 29776	Immunogencity: Tumor(100%, 3+ Cyto) Chronic pancreatitis(Variable to 1+ Cyto) Fibrotic stroma(Variable to 1+ Cyto) Specificity: High 4x 20x SF00029773	Immunogencity: Tumor(100%, 3+ Chronic pancreatitis(Variable to 2+ Fibrotic stroma(Variable to 2+ C Specificity: High 4x 20x SF00029774

FIG. 26-I

Cyto)	
Cyto) Cyto)	Immunogencity: N/A Specificity: N/A *SF00029779*
Cyto) Cyto)	
Cyto) yto)	
o 3+ Cyto) yto) Cyto)	
Cyto) Cyto) yto)	

FIG. 26-J

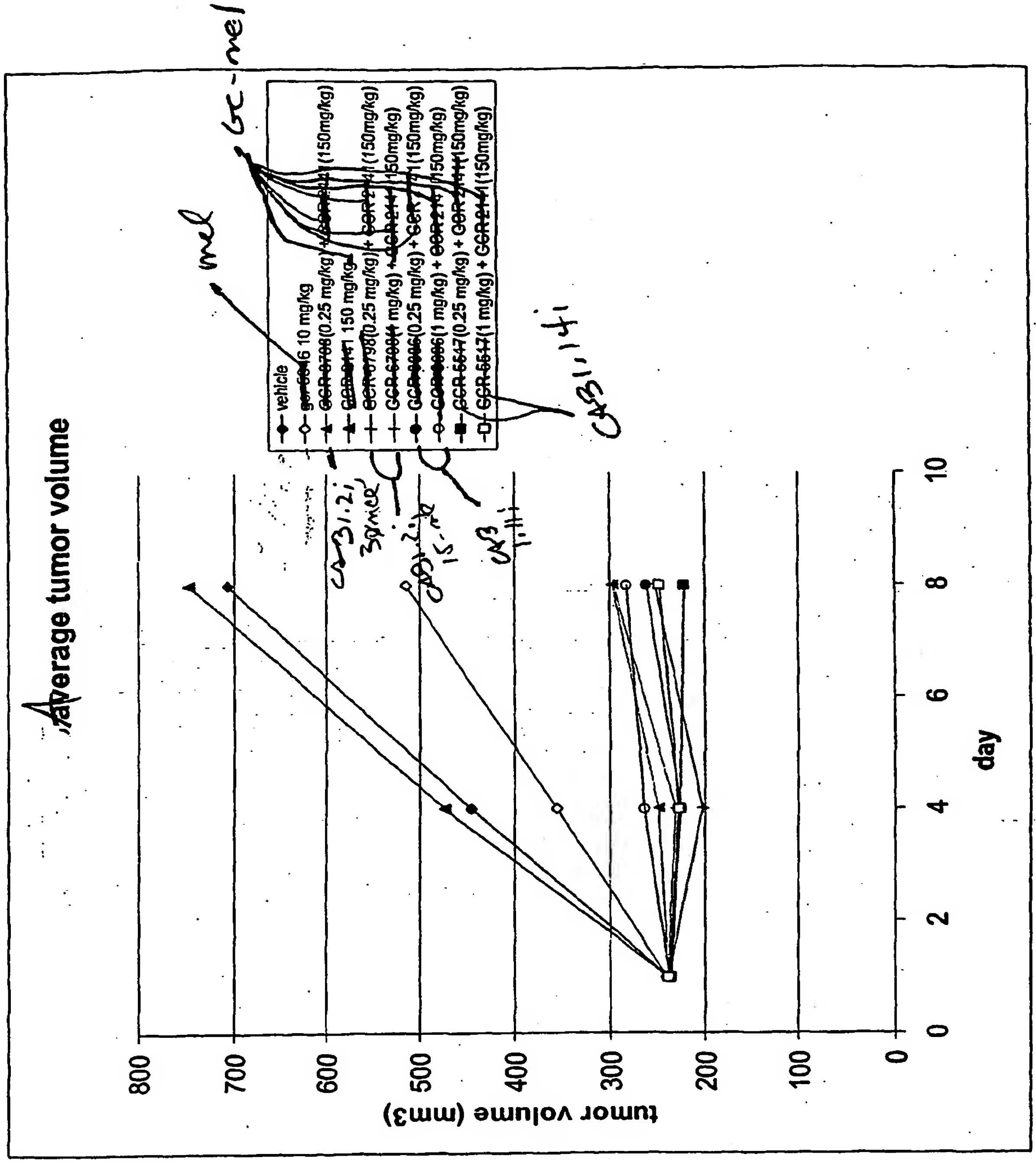

Average tumor volume
tumor volume (mm3)
800
700
600
500
400
300
200
100
0
0
2
4
6
8
10
day
vehicle
mel
GC-mel

FIGURE 27A

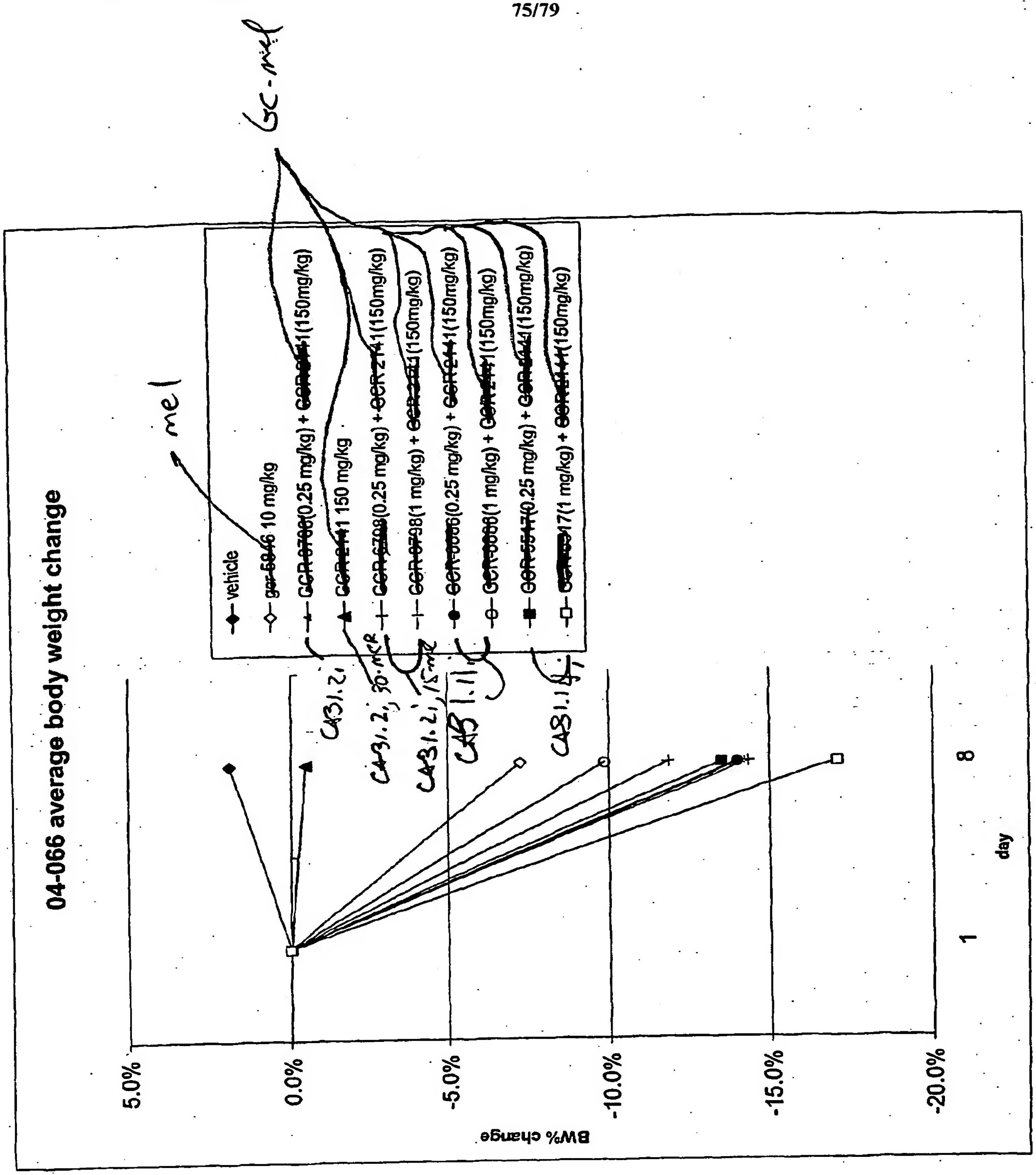
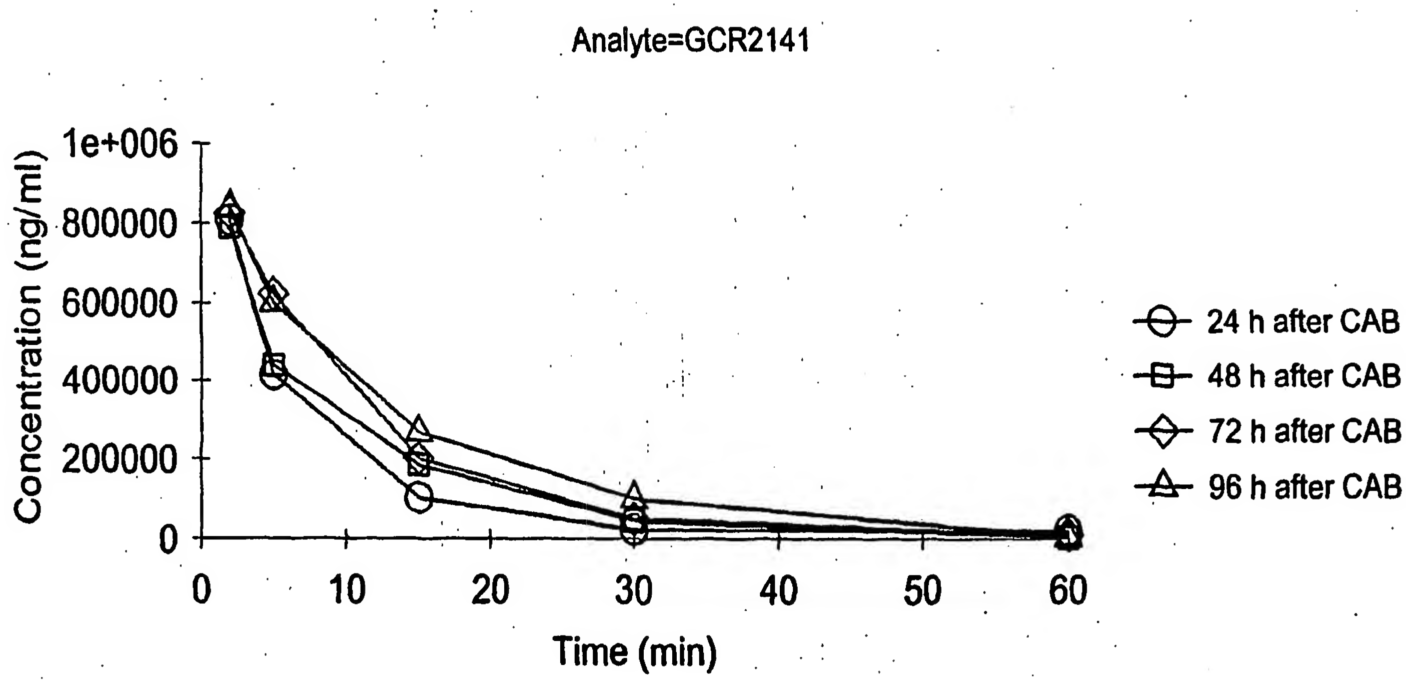

04-066 average body weight change
vehicle
ger 6846 10 mg/kg
GCR 6798(0.25 mg/kg) + GCR 2141(150mg/kg)
GCR 2141 150 mg/kg
GCR 6798(0.25 mg/kg) + GCR 2141(150mg/kg)
GCR 6798(1 mg/kg) + GCR 2141(150mg/kg)
GCR 6806(0.25 mg/kg) + GCR 2141(150mg/kg)
GCR 6806(1 mg/kg) + GCR 2141(150mg/kg)
GCR 5517(0.25 mg/kg) + GCR 2141(150mg/kg)
GCR 5517(1 mg/kg) + GCR 2141(150mg/kg)
mel
GC-mel
CAB1.2
CAB1.1
BW% change
5.0%
0.0%
-5.0%
-10.0%
-15.0%
-20.0%
1
8
day

FIGURE 27B

Figure 28

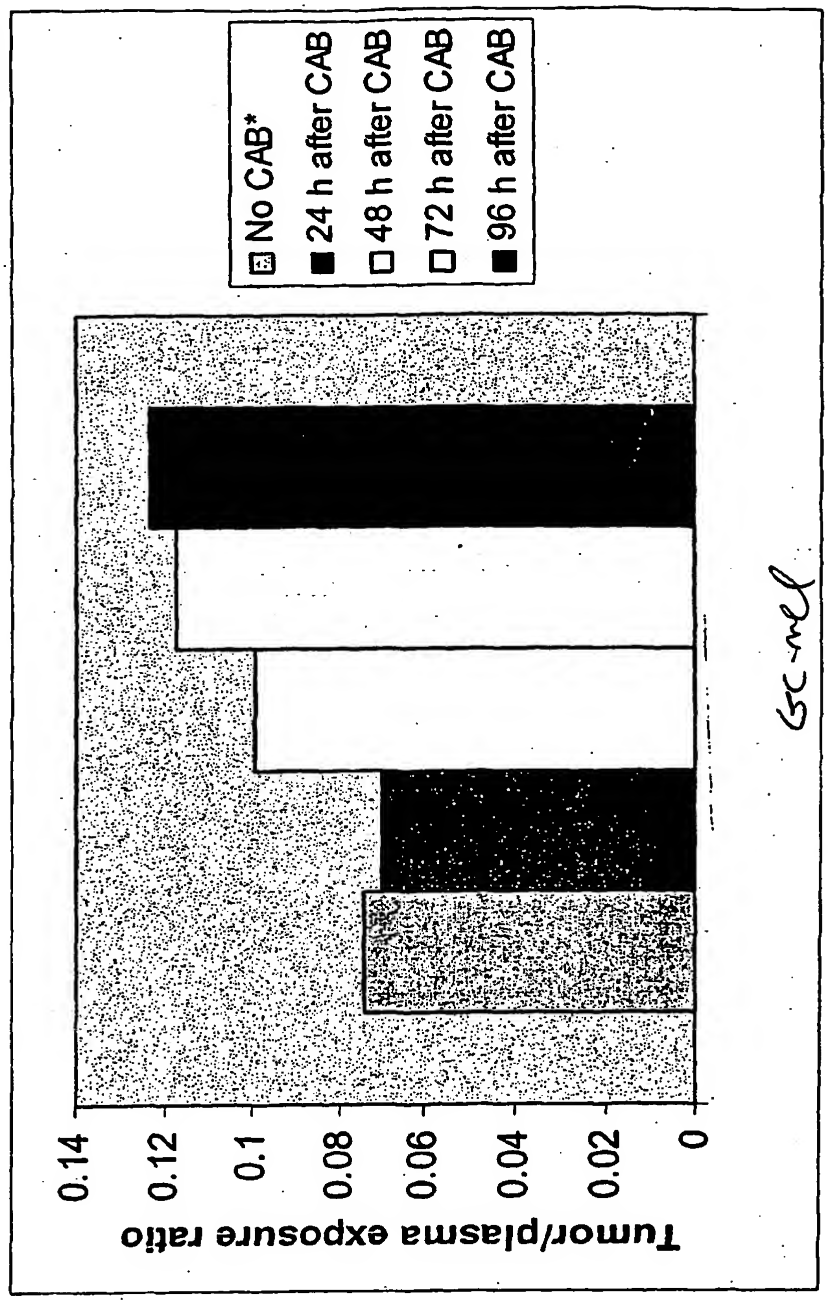
Plasma ~~GCR-2141~~ GC-Mel concentration-time profiles (linear-linear scale)



US04/41429

Tumor/Plasma GC-mel expo ratio

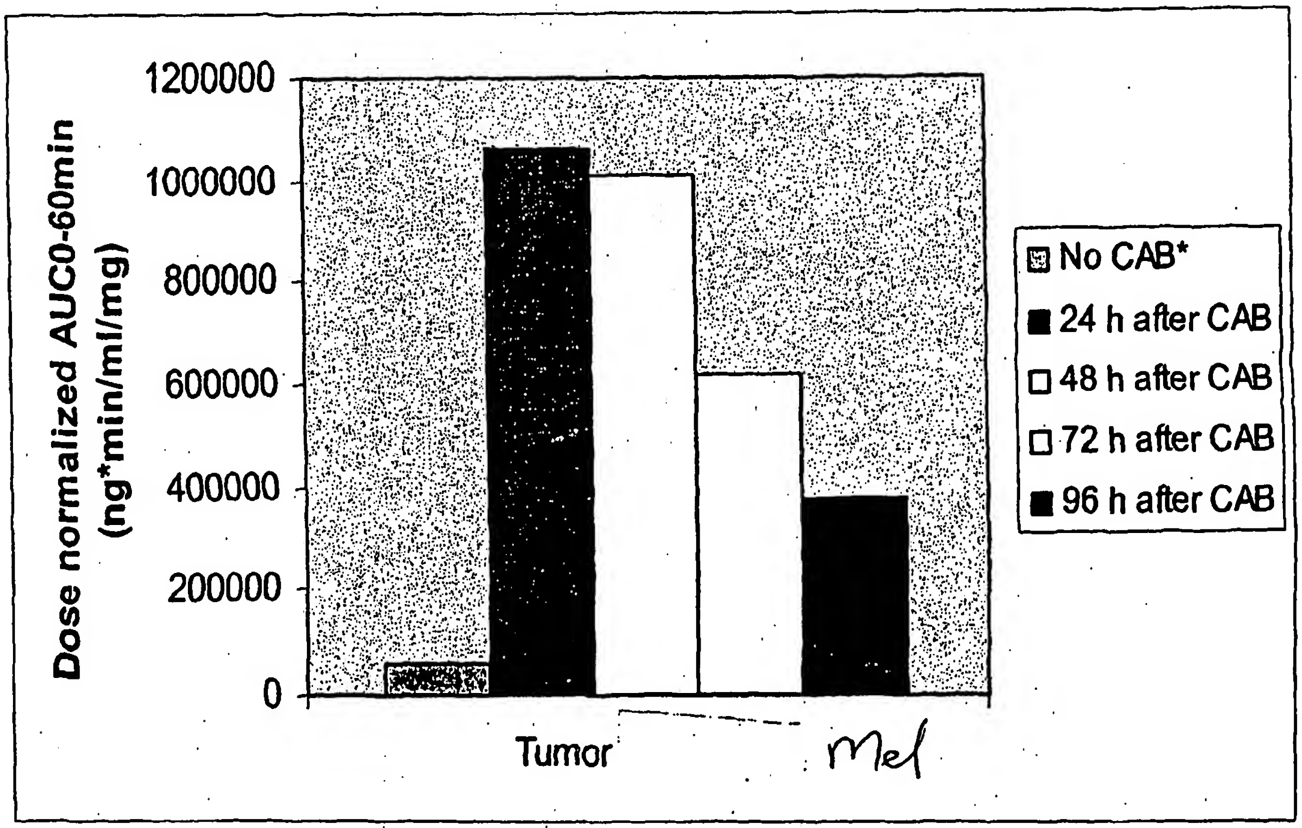
FIG 29A



Data from study 04052, melphalan formulated in cyclodextrin

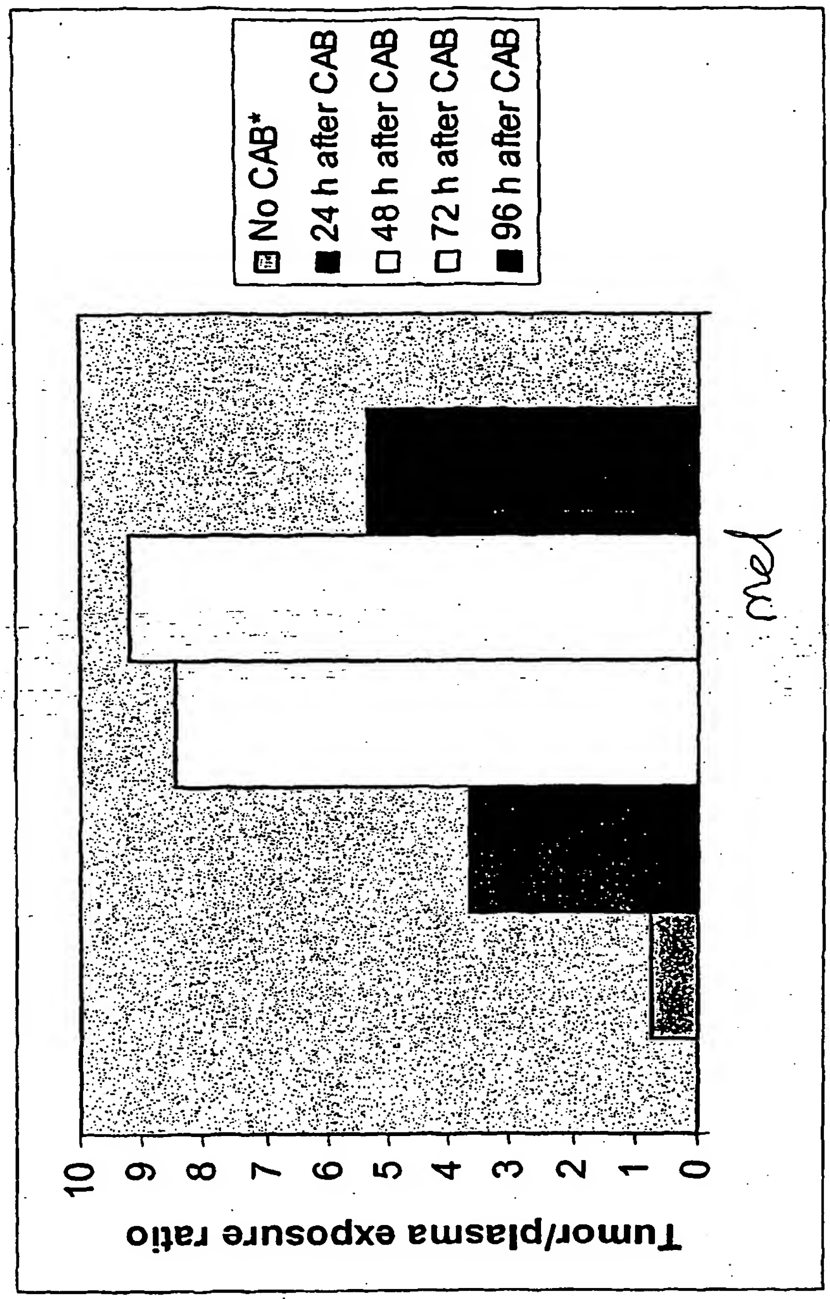
29 B

Tumor ~~GCP-5846~~ mel exposure after ~~GCP-2741~~ Gsc-mel administration



* Data from study 04052, melphalan formulated in cyclodextrin

FiG 29C - Tumor/plasma mel exposure after CAB after GC-mel ADMIN



* Data from study 04052, melphalan formulated in cyclodextrin